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München, den 1. Juli 2002
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CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL PROTEINS

Background of the Invention

5 Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic 10 compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have 15 been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

Summary of the Invention

20 This invention provides novel nucleic acid molecules which may be used to identify or classify *Corynebacterium glutamicum* or related species of bacteria. *C. glutamicum* is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The 25 nucleic acid molecules therefore can be used to identify microorganisms which can be used to produce fine chemicals, e.g., by fermentation processes. While *C. glutamicum* itself is nonpathogenic, it is related to other *Corynebacterium* species, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria), which are important human pathogens. The ability to identify the presence of *Corynebacterium* species 30 therefore also can have significant clinical relevance, e.g., diagnostic applications. Further, these nucleic acid molecules may serve as reference points for the mapping of the *C. glutamicum* genome, or of genomes of related organisms.

These novel nucleic acid molecules encode proteins, referred to herein as marker and fine chemical production (MCP) proteins. These MCP proteins may be involved, 35 for example, in the direct or indirect production of one or more fine chemicals from *C. glutamicum*. The MCP proteins of the invention may also participate in the degradation of hydrocarbons or the oxidation of terpenoids. These proteins may also be utilized for

the identification of *Corynebacterium glutamicum* or organisms related to *C. glutamicum*; the presence of an MCP protein specific to *C. glutamicum* and related species in a mixture of proteins may indicate the presence of one of these bacteria in the sample. Further, these MCP proteins may have homologues in plants or animals which 5 are involved in a disease state or condition; these proteins thus may serve as useful pharmaceutical targets for drug screening and the development of therapeutic compounds.

Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey et al., U.S. Patent No. 4,649,119, and 10 techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (e.g., *lactofermentum*) (Yoshihama et al. *J. Bacteriol.* 162: 591-597 (1985); Katsumata et al., *J. Bacteriol.* 159: 306-311 (1984); and Santamaria et al., *J. Gen Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to modulate the production of one or 15 more fine chemicals. This modulation may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation. For example, by modifying the activity of a protein involved in the biosynthesis or degradation of a fine chemical (i.e., through mutagenesis of the corresponding gene), one may directly modulate the ability of the cell to synthesize or to degrade this 20 compound, thereby modulating the yield and/or efficiency of production of the fine chemical. Similarly, by modulating the activity of a protein which regulates a fine chemical metabolic pathway, one may directly influence whether the production of the desired compound is up- or down-regulated, either of which will modulate the yield or efficiency of production of the fine chemical from the cell.

25 Indirect modulation of fine chemical production may also result by modifying the activity of a protein of the invention (i.e., by mutagenesis of the corresponding gene) such that the overall ability of the cell to grow and divide or to remain viable and productive is increased. The production of fine chemicals from *C. glutamicum* is generally accomplished by the large-scale fermentative culture of these microorganisms. 30 conditions which are frequently suboptimal for growth and cell division. By engineering a protein of the invention (e.g., a stress response protein, a cell wall protein, or proteins involved in the metabolism of compounds necessary for cell growth and division to occur, such as nucleotides and amino acids) such that it is better able to survive, grow, and multiply in such conditions, it may be possible to increase the number and productivity of such engineered *C. glutamicum* cells in large-scale culture, 35 which in turn should result in increased yields and/or efficiency of production of one or more desired fine chemicals. Further, the metabolic pathways of any cell are necessarily

interrelated and coregulated. By altering the activity or regulation of any one metabolic pathway in *C. glutamicum* (i.e., by altering the activity of one of the proteins of the invention which participates in such a pathway), it is possible to concomitantly alter the activity or regulation of other metabolic pathways in this microorganism, which may be directly involved in the synthesis or degradation of a fine chemical.

The invention provides novel nucleic acid molecules which encode proteins, referred to herein as MCP proteins, which are capable of, for example, modulating the production or efficiency of production of one or more fine chemicals from *C. glutamicum*, or of serving as identifying markers for *C. glutamicum* or related organisms. Nucleic acid molecules encoding an MCP protein are referred to herein as MCP nucleic acid molecules. In a preferred embodiment, the MCP protein is capable of modulating the production or efficiency of production of one or more fine chemicals from *C. glutamicum*, or of serving as identifying markers for *C. glutamicum* or related organisms. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (e.g., cDNAs) comprising a nucleotide sequence encoding an MCP protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of MCP-encoding nucleic acid (e.g., DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth in Appendix A or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth in Appendix A, or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth in Appendix B. The preferred MCP proteins of the present invention also preferably possess at least one of the MCP activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B, e.g., sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains an MCP activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to modulate the production or efficiency of production of one or more fine chemicals from *C. glutamicum*, or of

- serving as an identifying marker for *C. glutamicum* or related organisms. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%. 80% or 90% and most preferably at least about 95%. 96%. 97%. 98%, or 99% or more homologous to an amino acid sequence of Appendix B (e.g., an entire amino acid sequence selected from those sequences set forth in Appendix B). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).
- 10 In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (e.g., an MCP fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.
- 15 In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of Appendix A. Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* MCP protein, or a biologically active portion thereof.
- 20 25 Another aspect of the invention pertains to vectors, e.g., recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an MCP protein by culturing the host cell in a suitable medium. The MCP protein can then be isolated from the medium or the host cell.
- 30 35 Yet another aspect of the invention pertains to a genetically altered microorganism in which an MCP gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated MCP sequence as a transgene. In another embodiment, an endogenous MCP gene within the genome of the microorganism has been altered, e.g., functionally disrupted, by homologous recombination with an altered MCP gene. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with

Corynebacterium glutamicum being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

Still another aspect of the invention pertains to an isolated MCP protein or a portion, e.g., a biologically active portion, thereof. In a preferred embodiment, the isolated MCP protein or portion thereof is capable of modulating the production or efficiency of production of one or more fine chemicals from *C. glutamicum*, or of serving as an identifying marker for *C. glutamicum* or related organisms. In another preferred embodiment, the isolated MCP protein or portion thereof is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to, for example, modulate the production or efficiency of production of one or more fine chemicals from *C. glutamicum*, or to serve as identifying markers for *C. glutamicum* or related organisms.

The invention also provides an isolated preparation of an MCP protein. In preferred embodiments, the MCP protein comprises an amino acid sequence of Appendix B. In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame set forth in Appendix A). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of Appendix B. In other embodiments, the isolated MCP protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms.

Alternatively, the isolated MCP protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous, to a nucleotide sequence of Appendix B. It is also preferred that the preferred forms of MCP proteins also have one or more of the MCP bioactivities described herein.

The MCP polypeptide, or a biologically active portion thereof, can be operatively linked to a non-MCP polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the MCP

protein alone. In other preferred embodiments, this fusion protein is capable of modulating the yield, production and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, or of serving as an identifying marker for *C. glutamicum* or related organisms. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates production of a desired compound from the cell.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an MCP nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of 10 obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an MCP nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of 15 a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates MCP protein activity or MCP nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* 20 MCP protein activities, such that the yield, production, and/or efficiency of production of a desired fine chemical by this microorganism is improved. The agent which modulates MCP protein activity can be an agent which stimulates MCP protein activity or MCP nucleic acid expression. Examples of agents which stimulate MCP protein activity or MCP nucleic acid expression include small molecules, active MCP proteins, 25 and nucleic acids encoding MCP proteins that have been introduced into the cell. Examples of agents which inhibit MCP activity or expression include small molecules and antisense MCP nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields, 30 production, and/or efficiency of production of a desired compound from a cell, involving the introduction of a wild-type or mutant MCP gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a 35 preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides MCP nucleic acid and protein molecules. These MCP nucleic acid molecules may be utilized in the identification of *Corynebacterium glutamicum* or related organisms, in the mapping of the *C. glutamicum* genome (or a 5 genome of a closely related organism), or in the identification of microorganisms which may be used to produce fine chemicals, e.g., by fermentation processes. The proteins encoded by these nucleic acids may be utilized in the direct or indirect modulation of the production or efficiency of production of one or more fine chemicals from *C. glutamicum*, as identifying markers for *C. glutamicum* or related organisms, in the 10 oxidation of terpenoids or the degradation of hydrocarbons, or as targets for the development of therapeutic pharmaceutical compounds. Aspects of the invention are further explicated below.

I. Fine Chemicals

15 The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, 20 nucleosides, and nucleotides (as described e.g. in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm et al., eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (e.g., arachidonic acid), diols (e.g., propane diol, and butane diol), carbohydrates (e.g., hyaluronic acid and trehalose), aromatic compounds (e.g., aromatic amines, 25 vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research - 30 Asia, held Sept. 1-3, 1994 at Penang, Malaysia. AOCS Press. (1995)). enzymes, and all other chemicals described in Gutcho (1983) Chemicals by Fermentation. Noyes Data Corporation. ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

35 A. Amino Acid Metabolism and Uses

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-

recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ullmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L-optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins.

Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1983)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosynthesis, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino acids - technical production and use, p. 466-502 in Rehm et al. (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E. (1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α-

ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both 5 cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step 10 biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all 15 biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored. 20 and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. Biochemistry 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. 25 Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount 30 of that amino acid present in the cell.

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although 35 they are readily synthesized by other organisms such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of

metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry.

- 5 "Vitamins" vol. A27, p. 443-613. VCH: Weinheim, 1996.) The term "vitamin" is art-
recognized, and includes nutrients which are required by an organism for normal
functioning, but which that organism cannot synthesize by itself. The group of vitamins
may encompass cofactors and nutraceutical compounds. The language "cofactor"
includes nonproteinaceous compounds required for a normal enzymatic activity to
occur. Such compounds may be organic or inorganic; the cofactor molecules of the
10 invention are preferably organic. The term "nutraceutical" includes dietary supplements
having health benefits in plants and animals, particularly humans. Examples of such
molecules are vitamins, antioxidants, and also certain lipids (e.g., polyunsaturated fatty
acids).

- 15 The biosynthesis of these molecules in organisms capable of producing them,
such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial
Chemistry. "Vitamins" vol. A27, p. 443-613. VCH: Weinheim, 1996; Michal, G. (1999)
Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology. John Wiley
& Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and
20 Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological
Associations in Malaysia, and the Society for Free Radical Research - Asia, held Sept.
1-3, 1994 at Penang, Malaysia AOCS Press: Champaign, IL X, 374 S).

- 25 Thiamin (vitamin B₁) is produced by the chemical coupling of pyrimidine and
thiazole moieties. Riboflavin (vitamin B₂) is synthesized from guanosine-5'-triphosphate
(GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin
mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of
compounds collectively termed 'vitamin B₆' (e.g., pyridoxine, pyridoxamine, pyridoxa-
30 5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of
the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic
acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)-β-alanine) can be produced
either by chemical synthesis or by fermentation. The final steps in pantothenate
biosynthesis consist of the ATP-driven condensation of β-alanine and pantoic acid. The
enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β-
alanine and for the condensation to pantothenic acid are known. The metabolically
35 active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5
enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the
precursors of Coenzyme A. These enzymes not only catalyze the formation of

panthothenate, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B₅), pantetheine (and its derivatives) and coenzyme A.

- Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α-ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which is turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

- Corrinoids (such as the cobalamines and particularly vitamin B₁₂) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system. The biosynthesis of vitamin B₁₂ is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and niacinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

- The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B₆, pantothenate, and biotin. Only Vitamin B₁₂ is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

- Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid

moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are

- 5 nucleotides which may serve as energy stores (e.g., ADP, ATP) or as coenzymes (i.e., FAD and NAD).

Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (e.g. Christopherson,

R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine

- 10 biosynthesis as chemotherapeutic agents." *Med Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L. (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902).

- 15 However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (e.g., thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (e.g., ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (e.g., IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) *Nucleotides and*
- 20 *Related Compounds in Biotechnology* vol. 6. Rehm et al., eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: *Progress in Nucleic Acid Research and Molecular Biology*, vol. 42, Academic Press, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides". Chapter 8 in: *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York). Purine metabolism has been the subject of intensive research, and is

- 30 essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as
- 35 nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell.

Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP)

from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to 5 participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in a, α -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen 10 foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto et al., (1998) U.S. Patent No. 5.759.610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and 15 Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel 20 molecules, referred to herein as MCP nucleic acid molecules. These MCP nucleic acid molecules are useful not only for the identification of *C. glutamicum* or related bacterial species, but also as markers for the mapping of the *C. glutamicum* genome and in the identification of bacteria useful for the production of fine chemicals by, e.g., 25 fermentative processes. The present invention is also based, at least in part, on the MCP protein molecules encoded by these MCP nucleic acid molecules. These MCP proteins are capable of modulating the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, of serving as identifying markers for *C. glutamicum* or related organisms, of degrading hydrocarbons, and of serving as targets for the development of therapeutic pharmaceutical compounds. In one embodiment, the 30 MCP molecules of the invention directly or indirectly participate in one or more fine chemical metabolic pathways in *C. glutamicum*. In a preferred embodiment, the activity of the MCP molecules of the invention to indirectly or directly participate in such metabolic pathways has an impact on the production of a desired fine chemical by this microorganism. In a particularly preferred embodiment, the MCP molecules of the 35 invention are modulated in activity, such that the *C. glutamicum* metabolic pathways in which the MCP proteins of the invention participate are modulated in efficiency or

output, which either directly or indirectly modulates the production or efficiency of production of a desired fine chemical by *C. glutamicum*.

- The language, "MCP protein" or "MCP polypeptide" includes proteins which are able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target protein for drug screening or design, or to serve as identifying markers for *C. glutamicum* or related organisms. Examples of MCP proteins include those encoded by the MCP genes set forth in Table 1 and Appendix A. The terms "MCP gene" or "MCP nucleic acid sequence" include nucleic acid sequences encoding an MCP protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of MCP genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (e.g., kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (i.e., fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (e.g., the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound.

In another embodiment, the MCP molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*, either directly or indirectly. Using recombinant genetic techniques, one or more of the MCP proteins of the invention may be

manipulated such that its function is modulated. Such modulation of function may result in the modulation of the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*.

For example, by modifying the activity of a protein involved in the biosynthesis or degradation of a fine chemical (i.e., through mutagenesis of the corresponding gene), one may directly modulate the ability of the cell to synthesize or to degrade this compound, thereby modulating the yield and/or efficiency of production of the fine chemical. Similarly, by modulating the activity of a protein which regulates a fine chemical metabolic pathway, one may directly influence whether the production of the desired compound is up- or down-regulated, either of which will modulate the yield or efficiency of production of the fine chemical from the cell.

Indirect modulation of fine chemical production may also result by modifying the activity of a protein of the invention (i.e., by mutagenesis of the corresponding gene) such that the overall ability of the cell to grow and divide or to remain viable and productive is increased. The production of fine chemicals from *C. glutamicum* is generally accomplished by the large-scale fermentative culture of these microorganisms, conditions which are frequently suboptimal for growth and cell division. By engineering a protein of the invention (e.g., a stress response protein, a cell wall protein, or proteins involved in the metabolism of compounds necessary for cell growth and division to occur, such as nucleotides and amino acids) such that it is better able to survive, grow, and multiply in such conditions, it may be possible to increase the number and productivity of such engineered *C. glutamicum* cells in large-scale culture, which in turn should result in increased yields and/or efficiency of production of one or more desired fine chemicals. Further, the metabolic pathways of any cell are necessarily interrelated and coregulated. By altering the activity or regulation of any one metabolic pathway in *C. glutamicum* (i.e., by altering the activity of one of the proteins of the invention which participates in such a pathway), it is possible to concomitantly alter the activity or regulation of other metabolic pathways in this microorganism, which may be directly involved in the synthesis or degradation of a fine chemical.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequences of the isolated *C. glutamicum* MCP nucleic acid molecules and the predicted amino acid sequences of the *C. glutamicum* MCP proteins are shown in Appendices A and B, respectively. Computational analyses were performed which classified and/or identified many of these nucleotide sequences as sequences having homology to *E. coli* or *Bacillus subtilis* genes.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of Appendix B. As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the 5 selected amino acid sequence, e.g., the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid 10 sequence.

15 The MCP protein or a biologically active portion or fragment thereof of the invention is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms.

15 Various aspects of the invention are described in further detail in the following subsections:

A. Isolated Nucleic Acid Molecules

20 One aspect of the invention pertains to isolated nucleic acid molecules that encode MCP polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of MCP-encoding nucleic acid (e.g., MCP DNA). These nucleic acid molecules may be used to identify *C. glutamicum* or related organisms, to map the genome of *C. glutamicum* or closely related bacteria, or to identify microorganisms useful for the production of fine chemicals, e.g., by fermentative processes. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated 25 sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of 30 the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the 35

nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated MCP nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell

5 from which the nucleic acid is derived (e.g. a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, e.g., a nucleic acid molecule

10 having a nucleotide sequence of Appendix A, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* MCP cDNA can be isolated from a *C. glutamicum* library using all or portion of one of the sequences of Appendix A as a hybridization probe and standard hybridization techniques (e.g., as described in Sambrook, J., Fritsh, E. F., and

15 Maniatis, T. *Molecular Cloning. A Laboratory Manual*. 2nd. ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (e.g., a nucleic acid molecule encompassing

20 all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence of Appendix A). For example, mRNA can be isolated from normal endothelial cells (e.g., by the guanidinium-thiocyanate extraction procedure of Chirgwin et al. (1979) *Biochemistry* 18: 5294-5299) and cDNA can be prepared using reverse transcriptase

25 (e.g., Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL) and random polynucleotide primers or oligonucleotide primers based upon one of the nucleotide sequences shown in Appendix A. Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the

30 nucleotide sequences shown in Appendix A. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an MCP

35 nucleotide sequence can be prepared by standard synthetic techniques, e.g., using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in Appendix A. The sequences of Appendix A correspond to the *Corynebacterium glutamicum* MCP cDNAs of the invention. This cDNA comprises sequences encoding MCP proteins (i.e., "the coding region", indicated in each sequence in Appendix A), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in Appendix A. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in Appendix A.

For the purposes of this application, it will be understood that each of the sequences set forth in Appendix A has an identifying RXA number having the designation "RXA" followed by 5 digits (i.e., RXA00003). Each of these sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA designation to eliminate confusion. The recitation "one of the sequences in Appendix A", then, refers to any of the sequences in Appendix A, which may be distinguished by their differing RXA designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is set forth in Appendix B. The sequences of Appendix B are identified by the same RXA designations as Appendix A, such that they can be readily correlated. For example, the amino acid sequence in Appendix B designated RXA00003 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXA00003 in Appendix A.

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences shown in Appendix A, or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences shown in Appendix A is one which is sufficiently complementary to one of the nucleotide sequences shown in Appendix A such that it can hybridize to one of the nucleotide sequences shown in Appendix A, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50-60%, preferably at least about 60-70%, more preferably at least about 70-80%, 80-90%, or 90-95%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence shown in Appendix A, or a portion thereof. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a

nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to one of the nucleotide sequences shown in Appendix A, or a portion thereof.

- Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of one of the sequences in Appendix A, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an MCP protein. The nucleotide sequences determined from the cloning of the MCP genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning MCP homologues in other cell types and organisms, as well as MCP homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide.
- 10 The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the sequences set forth in Appendix A, an anti-sense sequence of one of the sequences set forth in Appendix A, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of Appendix A can be used in PCR reactions to clone MCP homologues. Probes based on the MCP nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, e.g. the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an MCP protein, such as by measuring a level of an MCP-encoding nucleic acid in a sample of cells, e.g., detecting MCP mRNA levels or determining whether a genomic MCP gene has been mutated or deleted.
- 20 25 In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (e.g., an amino acid residue which has a similar side chain as an amino acid residue in one of the sequences of Appendix B) amino acid residues to an amino acid sequence of Appendix B such that the protein or portion thereof is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C.*

5 *glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms. Examples of such activities are also described herein. Thus, "the function of an MCP protein" contributes to the overall regulation of one or more fine chemical metabolic pathways, or to the degradation of a hydrocarbon, or to the oxidation of a terpenoid.

In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B.

10 Portions of proteins encoded by the MCP nucleic acid molecules of the invention are preferably biologically active portions of one of the MCP proteins. As used herein, the term "biologically active portion of an MCP protein" is intended to include a portion, e.g., a domain/motif, of an MCP protein that modulates the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, that degrades hydrocarbons, that oxidizes terpenoids, that may serve as a target for drug development, or that may serve as an identifying marker for *C. glutamicum* or related organisms. To determine whether an MCP protein or a biologically active portion thereof can modulate the yield, production, and/or efficiency of production of one or 15 more fine chemicals from *C. glutamicum*, can degrade hydrocarbons, or can oxidize terpenoids, an assay of activity may be performed. Such assay methods are well known to those skilled in the art, as detailed in Example 8 of the Exemplification.

20 Additional nucleic acid fragments encoding biologically active portions of an MCP protein can be prepared by isolating a portion of one of the sequences in Appendix B, expressing the encoded portion of the MCP protein or peptide (e.g., by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the MCP protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown in Appendix A (and portions thereof) due to degeneracy 25 of the genetic code and thus encode the same MCP protein as that encoded by the nucleotide sequences shown in Appendix A. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in Appendix B. In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is 30 substantially homologous to an amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

In addition to the *C. glutamicum* MCP nucleotide sequences shown in Appendix A, it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of MCP proteins may exist within a population (e.g., the *C. glutamicum* population). Such genetic polymorphism in the 5 MCP gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an MCP protein, preferably a *C. glutamicum* MCP protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the MCP gene. Any and all such nucleotide variations and 10 resulting amino acid polymorphisms in MCP that are the result of natural variation and that do not alter the functional activity of MCP proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* MCP cDNA of the invention can be isolated based on their homology to the *C. glutamicum* MCP nucleic acid disclosed herein using the *C. glutamicum* cDNA, or a portion thereof, as a hybridization probe according to standard 15 hybridization techniques under stringent hybridization conditions. Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid 20 molecule comprising a nucleotide sequence of Appendix A. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are 25 such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those skilled in the art and can be found in *Current Protocols in Molecular Biology*. John Wiley & Sons. N.Y. (1989). 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization 30 conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C. followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a sequence of Appendix A corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an 35 RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* MCP protein.

In addition to naturally-occurring variants of the MCP sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into a nucleotide sequence of Appendix A, thereby leading to changes in the amino acid sequence of the encoded MCP protein, without altering the functional ability of the MCP protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a sequence of Appendix A. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the MCP proteins (Appendix B) without altering the activity of said MCP protein, whereas an "essential" amino acid residue is required for MCP protein activity. Other amino acid residues, however, (e.g., those that are not conserved or only semi-conserved in the domain having MCP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering MCP activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding MCP proteins that contain changes in amino acid residues that are not essential for MCP activity. Such MCP proteins differ in amino acid sequence from a sequence contained in Appendix B yet retain at least one of the MCP activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of Appendix B and is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to one of the sequences in Appendix B, more preferably at least about 60-70% homologous to one of the sequences in Appendix B, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of the sequences in Appendix B, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the sequences in Appendix B.

To determine the percent homology of two amino acid sequences (e.g., one of the sequences of Appendix B and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (e.g., one of the sequences of Appendix B) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (e.g., a mutant form of

the sequence selected from Appendix B), then the molecules are homologous at that position (i.e., as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences

5 (i.e., % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an MCP protein homologous to a protein sequence of Appendix B can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of Appendix A such that one or more amino acid substitutions, additions or deletions are introduced into the

10 encoded protein. Mutations can be introduced into one of the sequences of Appendix A by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is

15 one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g.,

lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid),

uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine,

20 proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an MCP protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly

25 along all or part of an MCP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an MCP activity described herein to identify mutants that retain MCP activity. Following mutagenesis of one of the sequences of Appendix A, the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of

30 the Exemplification).

In addition to the nucleic acid molecules encoding MCP proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, e.g.,

35 complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be

complementary to an entire MCP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an MCP protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are 5 translated into amino acid residues (e.g., the entire coding region of SEQ ID RXA00003 comprises nucleotides 1 to 741). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding MCP. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (i.e., also referred 10 to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding MCP disclosed herein (e.g., the sequences set forth in Appendix A), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of MCP mRNA, but 15 more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of MCP mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of MCP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed 20 by chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense 25 nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-

amino-3-N-2-carboxypropyl) uracil. (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e.. RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

5 The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an MCP protein to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecule to a peptide or 10 an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a eubacterial, 15 viral or eucaryotic promoter are preferred.

20 In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier et al. (1987) *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o- 25 methylribonucleotide (Inoue et al. (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue et al. (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a 30 ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave MCP mRNA transcripts to thereby inhibit translation of MCP mRNA. A ribozyme having specificity for an MCP-encoding nucleic acid can be designed based upon the nucleotide sequence of an MCP cDNA disclosed herein (i.e., 35 RXA00003 in Appendix A). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an MCP-encoding mRNA.

See, e.g., Cech et al. U.S. Patent No. 4,987,071 and Cech et al. U.S. Patent No. 5,116,742. Alternatively, MCP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

5 Alternatively, MCP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an MCP nucleotide sequence (e.g., an MCP promoter and/or enhancers) to form triple helical structures that prevent transcription of an MCP gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. et al. (1992) *Ann N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

10 *B. Recombinant Expression Vectors and Host Cells*

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an MCP protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

35 The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of

interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (e.g., in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, repressor binding sites, activator binding sites, enhancer regions and other expression control elements (e.g., terminators, other elements of mRNA secondary structure, or polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185. Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (e.g., MCP proteins, mutant forms of MCP proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of MCP proteins in prokaryotic or eukaryotic cells. For example, MCP genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. et al. (1992) "Foreign gene expression in yeast: a review". *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. et al. (1991) "Heterologous gene expression in filamentous fungi" in: *More Gene Manipulations in Fungi*. J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: *Applied Molecular Genetics of Fungi*. Peberdy, J.F. et al., eds., p. 1-28. Cambridge University Press: Cambridge). algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185. Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion

vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRJ75 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the MCP protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant MCP protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Arman et al., (1988) *Gene* 69:301-315) and pET 11d (Studier et al., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gnl0-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gnl). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gnl gene under the transcriptional control of the lacUV 5 promoter.

One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada et al. (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

- In another embodiment, the MCP protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYEpSec1 (Baldari, et al., (1987) *Embo J.* 6:229-234), pMFA (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz et al., (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi. in: Applied Molecular Genetics of Fungi. J.F. Peberdy, et al., eds., p. 1-28, Cambridge University Press: Cambridge.
- Alternatively, the MCP proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (e.g., Sf 9 cells) include the pAc series (Smith et al. (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).
- In another embodiment, the MCP proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (e.g., the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary Agrobacterium vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721.
- In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman et al. (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsch, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd. ed.. Cold Spring Harbor Laboratory. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.
- In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific: Pinkert et al.

(1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji et al. (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund et al. (1985) *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to MCP mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. et al. (1986) "Antisense RNA as a molecular tool for genetic analysis", *Reviews - Trends in Genetics*, Vol. 1(1).

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an MCP protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other

suitable host cells are known to those skilled in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

- Vector DNA can be introduced into prokaryotic or eukaryotic cells via
- 5 conventional transformation or transfection techniques. As used herein, the terms "transformation", "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (e.g., DNA) into a host cell, including using natural competence, chemical mediated transfer, calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated
- 10 transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, et al. (*Molecular Cloning. A Laboratory Manual. 2nd. ed. Cold Spring Harbor Laboratory*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

- For stable transfection of mammalian cells, it is known that, depending upon the
- 15 expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (e.g., resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418,
- 20 hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an MCP protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by, for example, drug selection (e.g., cells that have incorporated the selectable marker gene will survive, while the other cells die).

- 25 To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an MCP gene into which a deletion, addition or substitution has been introduced to thereby alter, e.g., functionally disrupt, the MCP gene. Preferably, this MCP gene is a *Corynebacterium glutamicum* MCP gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source.
- 30 In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous MCP gene is functionally disrupted (i.e., no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous MCP gene is mutated or otherwise altered but still encodes functional protein (e.g., the upstream regulatory region can be altered to thereby alter the expression of the endogenous MCP protein). In the homologous recombination vector, the altered portion of the MCP gene is flanked at its 5' and 3' ends by additional nucleic acid of the MCP
- 35

gene to allow for homologous recombination to occur between the exogenous MCP gene carried by the vector and an endogenous MCP gene in a microorganism. The additional flanking MCP nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, less than one kilobase of flanking DNA (both at the 5' and 3' ends) is included in the vector (see e.g., Thomas, K.R. and 5 Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (e.g., by electroporation) and cells in which the introduced MCP gene has homologously recombined with the endogenous MCP gene are selected using art-known techniques.

10 In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of an MCP gene on a vector placing it under control of the lac operon permits expression of the MCP gene in the presence of IPTG. Such regulatory systems are well known in the art.

15 A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (i.e., express) an MCP protein. Accordingly, the invention further provides methods for producing MCP proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an MCP protein has 20 been introduced, or into which genome has been introduced a gene encoding a wild-type or altered MCP protein) in a suitable medium until MCP protein is produced. In another embodiment, the method further comprises isolating MCP proteins from the medium or the host cell.

25 C. Isolated MCP Proteins

Another aspect of the invention pertains to isolated MCP proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when 30 chemically synthesized. The language "substantially free of cellular material" includes preparations of MCP protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of MCP protein having less than about 30% (by dry weight) of non-MCP protein (also referred to herein 35 as a "contaminating protein"), more preferably less than about 20% of non-MCP protein, still more preferably less than about 10% of non-MCP protein, and most preferably less than about 5% non-MCP protein. When the MCP protein or biologically active portion

thereof is recombinantly produced, it is also preferably substantially free of culture medium, i.e., culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of MCP protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of MCP protein having less than about 30% (by dry weight) of chemical precursors or non-MCP chemicals, more preferably less than about 20% chemical precursors or non-MCP chemicals, still more preferably less than about 10% chemical precursors or non-MCP chemicals, and most preferably less than about 5% chemical precursors or non-MCP chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the MCP protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* MCP protein in a microorganism such as *C. glutamicum*.

An isolated MCP protein or a portion thereof of the invention is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an MCP protein of the invention has an amino acid sequence shown in Appendix B. In yet another preferred embodiment, the MCP protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to a nucleotide sequence of Appendix A. In still another preferred embodiment, the MCP protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50-60%, preferably at least about 60-70%, more preferably at least about 70-80%, 80-90%, 90-95%, and even more preferably at least about 96%, 97%, 98%, 99% or more homologous to one of the amino acid sequences of Appendix B. The preferred MCP proteins of the present invention also preferably possess at least one of the MCP

activities described herein. For example, a preferred MCP protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to a nucleotide sequence of Appendix A, and which is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms.

In other embodiments, the MCP protein is substantially homologous to an amino acid sequence of Appendix B and retains the functional activity of the protein of one of the sequences of Appendix B yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the MCP protein is a protein which comprises an amino acid sequence which is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80, 80-90, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B and which has at least one of the MCP activities described herein. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B.

Biologically active portions of an MCP protein include peptides comprising amino acid sequences derived from the amino acid sequence of an MCP protein, e.g., an amino acid sequence shown in Appendix B or the amino acid sequence of a protein homologous to an MCP protein, which include fewer amino acids than a full length MCP protein or the full length protein which is homologous to an MCP protein, and exhibit at least one activity of an MCP protein. Typically, biologically active portions (peptides, e.g., peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an MCP protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an MCP protein include one or more selected domains/motifs or portions thereof having biological activity.

MCP proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the MCP protein is expressed in the host cell. The MCP protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an MCP protein,

polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native MCP protein can be isolated from cells (e.g., endothelial cells, bacterial cells, fungal cells or other cells), for example using an anti-MCP antibody, which can be produced by standard techniques utilizing an MCP protein or fragment thereof of this invention.

The invention also provides MCP chimeric or fusion proteins. As used herein, an MCP "chimeric protein" or "fusion protein" comprises an MCP polypeptide operatively linked to a non-MCP polypeptide. An "MCP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an MCP protein, whereas a "non-MCP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the MCP protein, e.g., a protein which is different from the MCP protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the MCP polypeptide and the non-MCP polypeptide are fused in-frame to each other. The non-MCP polypeptide can be fused to the N-terminus or C-terminus of the MCP polypeptide. For example, in one embodiment the fusion protein is a GST-MCP fusion protein in which the MCP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant MCP proteins. In another embodiment, the fusion protein is an MCP protein containing a heterologous signal sequence at its N-terminus. In certain host cells (e.g., mammalian host cells, bacterial host cells, fungal host cells), expression and/or secretion of an MCP protein can be increased through use of a heterologous signal sequence.

Preferably, an MCP chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel et al. John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). An MCP-

encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the MCP protein.

Homologues of the MCP protein can be generated by mutagenesis, e.g., discrete point mutation or truncation of the MCP protein. As used herein, the term "homologue" refers to a variant form of the MCP protein which acts as an agonist or antagonist of the activity of the MCP protein. An agonist of the MCP protein can retain substantially the same, or a subset, of the biological activities of the MCP protein. An antagonist of the MCP protein can inhibit one or more of the activities of the naturally occurring form of the MCP protein, by, for example, competitively binding to a downstream or upstream member of a biochemical pathway which includes the MCP protein.

In an alternative embodiment, homologues of the MCP protein can be identified by screening combinatorial libraries of mutants, e.g., truncation mutants, of the MCP protein for MCP protein agonist or antagonist activity. In one embodiment, a variegated library of MCP variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of MCP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential MCP sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g., for phage display) containing the set of MCP sequences therein.

There are a variety of methods which can be used to produce libraries of potential MCP homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential MCP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, e.g., Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura et al. (1984) *Annu. Rev. Biochem.* 53:323; Itakura et al. (1984) *Science* 198:1056; Ike et al. (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the MCP protein coding can be used to generate a variegated population of MCP fragments for screening and subsequent selection of homologues of an MCP protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an MCP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression

vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the MCP protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of MCP homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify MCP homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave et al. (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated MCP library, using methods well known in the art.

20 D. *Uses and Methods of the Invention*

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of MCP protein regions required for function; modulation of an MCP protein activity; modulation of the activity of one or more metabolic pathways; and modulation of cellular production of a desired compound, such as a fine chemical.

30 The MCP nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes, and probes based thereon; by probing the extracted genomic DNA of a culture of a unique or mixed 35 population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is

nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*. Detection of such organisms is of significant clinical relevance.

To detect the presence of *C. glutamicum* in a sample, techniques well known in the art may be employed. Specifically, the cells in the sample may optionally first be

- 5 cultured in a suitable liquid or on a suitable solid culture medium to increase the number of cells in the sample. These cells are lysed, and the total DNA content extracted and optionally purified to remove debris and protein material which may interfere with subsequent analysis. The polymerase chain reaction or a similar technique known in the art is performed (for general reference on methodologies commonly used for the
10 amplification of nucleic acid sequences, see Mullis et al., U.S. Patent No. 4,683,195, Mullis et al., U.S. Patent No. 4,965,188, and Innis, M.A., and Gelfand, D. H., (1989) PCR Protocols, A guide to Methods and Applications, Academic Press, p. 3-12, and (1988) Biotechnology 6:1197, and International Patent Application No. WO89/01050)
in which primers specific to an MCP nucleic acid molecule of the invention are
15 incubated with the nucleic acid sample such that, if present in the sample, that particular MCP nucleic acid sequence will be amplified. The particular MCP nucleic acid to be amplified is selected based on its uniqueness to the *C. glutamicum* genome, or to the genomes of *C. glutamicum* and only a few closely related bacteria. The presence of the desired amplified product is thus indicative of the presence of *C. glutamicum*, or an
20 organism closely related to *C. glutamicum*.

Further, the nucleic acid and protein molecules of the invention may serve as markers for specific regions of the genome. It is possible, using techniques well known in the art, to ascertain the physical location on the *C. glutamicum* genome of the MCP nucleic acid molecules of the invention, which in turn provides markers on the genome which can be used to aid in the placement of other nucleic acid molecules and genes on the genome map. Also, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related bacterial species that these nucleic acid molecules may similarly permit the construction of a genomic map in such bacteria (e.g., *Brevibacterium lactofermentum*).

- 30 The nucleic acid molecules of the invention have utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed
35 with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed

multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds.

The MCP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

The MCP protein molecules of the invention may also be utilized as markers for the classification of an unknown bacterium as *C. glutamicum*, or for the identification of *C. glutamicum* or closely related bacteria in a sample. For example, using techniques well known in the art, cells in a sample may optionally be amplified (e.g., by culturing in an appropriate medium) to increase the sample size, and then may be lysed to release proteins contained therein. This sample may optionally be purified to remove debris and nucleic acid molecules which may interfere with subsequent analysis. Antibodies specific for a selected MCP protein of the invention may be incubated with the protein sample in a typical Western assay format (see, e.g., Ausubel et al., (1988) Current Protocols in Molecular Biology, Wiley: New York) in which the antibody will bind to its target protein if this protein is present in the sample. An MCP protein is selected for this type of assay if it is unique or nearly unique to *C. glutamicum* or *C. glutamicum* and bacteria very closely related to *C. glutamicum*. Proteins in the sample are then separated by gel electrophoresis, and transferred to a suitable matrix, such as nitrocellulose. An appropriate secondary antibody having a detectable label (e.g., chemiluminescent or colorimetric) is incubated with this matrix, followed by stringent washing. The presence or absence of the label is indicative of the presence or absence of the target protein in the sample. If the protein is present, then this is indicative of the presence of *C. glutamicum*. A similar process enables the classification of an unknown bacterium as *C. glutamicum*; if a panel of proteins specific to *C. glutamicum* are not detected in protein samples prepared from the unknown bacterium, then that bacterium is not likely to be *C. glutamicum*.

Genetic manipulation of the MCP nucleic acid molecules of the invention may result in the production of MCP proteins having functional differences from the wild-

type MCP proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

- Such changes in activity may directly modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*. For example, by modifying the activity of a protein involved in the biosynthesis or degradation of a fine chemical (i.e., through mutagenesis of the corresponding gene), one may directly modulate the ability of the cell to synthesize or to degrade this compound, thereby modulating the yield and/or efficiency of production of the fine chemical. Similarly, by modulating the activity of a protein which regulates a fine chemical metabolic pathway, one may directly influence whether the production of the desired compound is up- or down-regulated, either of which will modulate the yield or efficiency of production of the fine chemical from the cell.

- Indirect modulation of fine chemical production may also result by modifying the activity of a protein of the invention (i.e., by mutagenesis of the corresponding gene) such that the overall ability of the cell to grow and divide or to remain viable and productive is increased. The production of fine chemicals from *C. glutamicum* is generally accomplished by the large-scale fermentative culture of these microorganisms, conditions which are frequently suboptimal for growth and cell division. By engineering a protein of the invention (e.g., a stress response protein, a cell wall protein, or proteins involved in the metabolism of compounds necessary for cell growth and division to occur, such as nucleotides and amino acids) such that it is better able to survive, grow, and multiply in such conditions, it may be possible to increase the number and productivity of such engineered *C. glutamicum* cells in large-scale culture, which in turn should result in increased yields and/or efficiency of production of one or more desired fine chemicals. Further, the metabolic pathways of any cell are necessarily interrelated and coregulated. By altering the activity or regulation of any one metabolic pathway in *C. glutamicum* (i.e., by altering the activity of one of the proteins of the invention which participates in such a pathway), it is possible to concomitantly alter the activity or regulation of other metabolic pathways in this microorganism, which may be directly involved in the synthesis or degradation of a fine chemical.

- The aforementioned mutagenesis strategies for MCP proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one skilled in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated MCP nucleic acid and protein molecules such that

the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any natural product of *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, and published patent applications cited throughout this application are hereby incorporated by reference.

5

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum*

ATCC 13032

- 10 A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation. the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose.
- 15 2.46 g/l MgSO₄ x 7H₂O, 10 ml/l KH₂PO₄ solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l (NH₄)₂SO₄, 1 g/l NaCl, 2 g/l MgSO₄ x 7H₂O, 0.2 g/l CaCl₂, 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l FeSO₄ x H₂O, 10 mg/l ZnSO₄ x 7 H₂O, 3 mg/l MnCl₂ x 4 H₂O, 30 mg/l H₃BO₃, 20 mg/l CoCl₂ x 6 H₂O, 1 mg/l NiCl₂ x 6 H₂O, 3 mg/l Na₂MoO₄ x 2 H₂O, 500 mg/l complexing agent
- 20 (EDTA or citric acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting
- 25 protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca. 18 h at 37°C. The DNA was purified by extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20

μg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30 min incubation at -20°C, the DNA was collected by centrifugation (13.000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

5 **Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.**

10 Starting from DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (see e.g., Sambrook, J. et al. (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. et al. (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

15 Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) Proc. Natl. Acad. Sci. USA, 75:3737-3741); pACYC177 (Change & Cohen (1978) J. Bacteriol 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or 20 Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) Gene 53:283-286.

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using 25 ABI377 sequencing machines (see e.g., Fleischman, R.D. et al. (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd.", Science, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

30 **Example 4: *In vivo* Mutagenesis**

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (e.g. *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain

the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (e.g., mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294. ASM: Washington.) Such strains are well known to those skilled in the art. The use of such strains is 5 illustrated, for example, in Greener, A. and Callahan, M. (1994) Strategies 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous 10 plasmids (as e.g., pHM1519 or pBL1) which replicate autonomously (for review see, e.g., Martin, J.F. et al. (1987) Biotechnology, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for 15 *E. coli* (Sambrook, J. et al. (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. et al. (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin of replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are 20 genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see e.g., Yoshihama, M. et al. (1985) J. Bacteriol. 162:591-597, 25 Martin J.F. et al. (1987) Biotechnology, 5:137-146 and Eikmanns, B.J. et al. (1991) Gene. 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by 30 protoplast transformation (Kastsumata, R. et al. (1984) J. Bacteriol. 159:306-311), electroporation (Liebl, E. et al. (1989) FEMS Microbiol. Letters, 53:399-303) and in cases where special vectors are used, also by conjugation (as described e.g. in Schäfer, A et al. (1990) J. Bacteriol. 172:1663-1666). It is also possible to transfer the shuttle vectors for

000-017-900
C. glutamicum to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an *Mcr*-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) J. Mol. Biol. 166:1-19).

5 **Example 6: Assessment of the Expression of the Mutant Protein**

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel et al. (1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. et al. (1992) Mol. Microbiol. 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel et al. (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) Appl. Microbiol. Biotechnol., 32:205-210; von der Osten *et al.* (1998) Biotechnology Letters, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Prokaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as NH₄Cl or (NH₄)₂SO₄, NH₄OH, nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuic acid, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A Practical Approach (eds. P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0

19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (brain heart infusion, DIFC) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to 10 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media.

An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It is also possible to maintain a constant culture pH through the addition of NaOH or NH₄OH during growth. If complex medium components such as yeast extract are utilized, 15 the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the 20 broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes. For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 25 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control 30 clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD₆₀₀ of 0.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2.5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract,

22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

5 Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one skilled in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be found, for example, in the following references: Dixon, M.. and Webb, E.C., (1979) Enzymes. Longmans: London; Fersht, (1985) Enzyme Structure and Mechanism. Freeman: New York; Walsh, (1979) Enzymatic Reaction Mechanisms. Freeman: San Francisco; Price, N.C.. Stevens, L. (1982) Fundamentals of Enzymology. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) The Enzymes, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) Enzymkinetik. 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) Methods of Enzymatic Analysis, 3rd ed., vol. I-XII. Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim. p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. et al. (1995) EMBO J. 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in Biomembranes, Molecular Structure and Function, Springer: Heidelberg. p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing

- the medium and/or the cellular component for increased production of the desired product (i.e., an amino acid). Such analysis techniques are well known to one skilled in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography
- 5 such as high performance liquid chromatography (see, for example, Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. et al., (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm et al. (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page
- 10 469-714, VCH: Weinheim; Belter, P.A. et al. (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ullmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow.
- 15 F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (e.g., sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

- 30 Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

- The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One skilled in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified.
- 10 The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. Biochemical Engineering Fundamentals, McGraw-Hill: New York (1986).

- 15 The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek et al. (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova et al. (1996) *Biotehnologiya* 11: 27-32; and Schmidt et al. (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley and Sons; Fallon, A. et al. (1987) Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17.

Equivalents

- Those skilled in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

TABLE 1: GENES IN THE APPLICATION

<u>Identification</u>	<u>Code</u>	<u>Config</u>	<u>NT</u>	<u>NT</u>
			<u>Start</u>	<u>Stop</u>
RXA0223	CR00852	CR00041	425	6
RXA00911	CR00248	CR00041	1259	1705
RXA02032	CR00818	CR00041	4160	4729
RXA01707	CR000481	CR000481	802	1628
RXA00271	CR00041	CR00041	709	2720
RXA02427	CR00707	CR00707	3447	3061
RXA00199	CR00087	CR00087	830	1144
RXA01186	CR00338	CR00338	3742	2645
RXA00150	CR00023	CR00023	4085	4850
RXA00016	CR00035	CR00035	420	635
RXA00138	CR00059	CR00059	1	783
RXA00555	CR00145	CR00145	2555	1665
RXA01657	CR00169	CR00169	10082	9940
RXA00890	CR00253	CR00253	3841	3089
RXA01198	CR00343	CR00343	3422	3724
RXA01508	CR00443	CR00443	497	33
RXA01691	CR00474	CR00474	1553	2974
RXA02425	CR00707	CR00707	1	630
RXA02573	CR00739	CR00739	594	151
RXA02865	CR00753	CR00753	8497	8018
RXA00889	CR00242	CR00242	15341	15928
RXA02808	CR00187	CR00187	48	570
RXA01658	CR00460	CR00460	1548	2444
RXA02721	CR00159	CR00159	1373	636
RXA00462	CR00116	CR00116	3023	1644
RXA01286	CR00307	CR00307	14437	13423
RXA01380	CR00403	CR00403	2	2017
RXA02520	CR00725	CR00725	7943	8071
RXA00027	CR00003	CR00003	5142	5507
RXA00117	CR00019	CR00019	791	201
RXA00247	CR00037	CR00037	7097	6171
RXA01815	CR00515	CR00515	3294	4085
RXA02138	CR00639	CR00639	4409	4750
RXA07107	CR00632	CR00632	1536	1877
RXA02180	CR00841	CR00841	16813	16356
RXA01986	CR00587	CR00587	47	703
RXA00411	CR00092	CR00092	1685	1011
RXA01982	CR00573	CR00573	3001	1844

<u>Identification Code</u>	<u>Config.</u>	<u>NT Start</u>	<u>NT Stop</u>
RXA02387	GR00687	2182	1554
RXA02884	GR10070	1695	2156
RXA02771	GR00762	8407	8027
RXA02840	GR00835	488	339
RXA01986	GR00585	88	824
RXA01985	GR00343	1413	1859
RXA01986	GR00561	1257	826
RXA01985	GR00692	608	6
RXA001305	GR00763	777	4534
RXA02387	GR00016	5118	76
RXA02735	GR00035	546	13405
RXA02209	GR00755	14502	1177
RXA01091	GR00754	593	
RXA02680	GR00175	2851	104
RXA00867	GR00070	1284	877
RXA00358	GR00185	5283	6911
RXA00678	GR00188		
RXA01719			9869
		10574	2830
	GR00456	1733	1081
	GR00827	3	2633
	GR00066	1548	511
	GR00688	113	7231
	GR00023	7656	3100
	GR00093	404	7771
	GR00109	6818	9238
	GR00057	8594	1848
	GR00241	758	1860
	GR00700	656	21656
	GR00387	23467	18526
	GR000367	19365	10695
	GR001271	11513	1468
	GR00458	854	2938
	GR00466	2037	115
	GR00215	806	8038
	GR00002	6857	431
	GR00393	6	3355
	GR00235	4374	13580
	GR00300	12038	203
	GR00654		
	GR00475	799	
	GR00728	18749	12924
	GR00754	12268	13084
	GR01754	13405	12354
	GR01754	13037	1919
	GR00741	1518	9185
	GR00397	8811	800
	GR00438	12268	13330
	GR00441	6133	6133
	GR00423		
	GR00447		
	GR00192		

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<u>Identification Code</u>	<u>Config.</u>	NT <u>Start</u>	NT <u>Stop</u>
RXA01597	GR00447	6220	1401
RXA01176	GR00335	1980	1477
RXA01740	GR00495	3681	4460
RXA02137	GR00839	4166	3369
RXA02141	GR00839	8457	8884
RXA02076	GR00628	6902	7435
RXA00473	GR00119	5788	6563
RXA02121	GR00046	420	4
RXA00234	GR00018	998	459
RXA00161	GR00024	4893	5354
RXA00183	GR00028	7144	8195
RXA00279	GR00043	4001	2816
RXA00474	GR00119	6575	8152
RXA02314	GR00885	8179	5939
RXA00560	GR00149	256	492
RXA00587	GR00156	13008	12490
RXA02375	GR00719	1907	3064
RXA02824	GR00805	531	4
RXA02849	GR00849	2	283
RXA01159	GR00328	3089	2775
RXA01023	GR00292	1817	867
RXA01944	GR00558	2	385
RXA01635	GR00454	5575	8315
RXA01638	GR00454	6326	6898
RXA01945	GR00558	392	1633
RXA01968	GR00587	3295	2138
RXA02452	GR00710	5271	5092
RXA02183	GR00864	18663	19187
RXA00614	GR00162	1680	2594
RXA01322	GR00385	443	6
RXA01142	GR00389	11296	12807
RXA00054	GR00098	8557	11469
RXA00398	GR00014	4146	5048
RXA00397	GR00014	5222	6182
RXA00118	GR00019	918	1172
RXA00122	GR00019	4220	5842
RXA00134	GR00021	1648	1019
RXA00159	GR00024	3868	2687
RXA00165	GR00028	9418	12045
RXA00220	GR00032	20866	20163
RXA00248	GR00037	7843	7121
RXA00285	GR00048	3	515
RXA00321	GR00057	2411	597
RXA00322	GR00057	3658	2555
RXA00339	GR00059	817	1533
RXA00396	GR00086	6653	8163
RXA00422	GR00097	428	6

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<u>Identification</u>	<u>NT</u>	<u>Stop</u>
<u>Code</u>	<u>Start</u>	<u>Config.</u>
RXA00428	GR00098	2657
RXA00491	CR00122	1057
RXA00105	CR00126	252
RXA00540	CR00139	2027
RXA00552	CR00145	2
RXA00553	CR00145	718
RXA00573	CR00158	742
RXA00574	CR00158	117
RXA00578	CR00156	767
RXA00586	CR00156	4087
RXA00610	CR00156	12818
RXA00613	CR00161	11937
RXA00617	CR00162	1082
RXA00713	CR00162	1652
RXA00716	CR00167	1200
RXA00849	CR00168	2002
RXA00886	CR00169	2754
RXA00891	CR00175	2823
RXA00911	CR00181	3278
RXA00913	CR00181	390
RXA00913	CR00181	4
RXA00917	CR00188	2152
RXA00916	CR00188	71
RXA00922	CR00189	1033
RXA00922	CR00189	3514
RXA00938	CR00201	1015
RXA00955	CR00204	78
RXA00955	CR00204	3283
RXA00957	CR00204	71
RXA00968	CR00204	1033
RXA00971	CR00206	512
RXA00978	CR00206	5956
RXA00985	CR00206	6399
RXA00985	CR00206	2395
RXA00981	CR00230	782
RXA00946	CR00230	782
RXA00959	CR00234	5
RXA00969	CR00239	4
RXA00987	CR00242	636
RXA00940	CR00257	13544
RXA00949	CR00259	792
RXA00986	CR00280	14266
RXA00997	CR00280	129
RXA01011	CR00288	524
RXA01017	CR00290	5400
RXA01021	CR00291	8047
RXA01074	CR00300	60
RXA01078	CR00300	401
RXA01086	CR00304	41
RXA01129	CR00314	2107
RXA01198	CR00343	875
RXA01197	CR00343	1
RXA01207	CR00347	792
RXA01237	CR00358	2089
RXA01240	CR00360	1902
RXA01249	CR00363	1567
RXA01251	CR00365	2111
RXA01282	CR00389	1759
RXA01294	CR00373	2280
RXA01348	CR00392	2482
RXA01357	CR00393	4
		536
		4685
		3537
		2872
		752
		4659

<u>Identification Code</u>	<u>Contdg.</u>	<u>NT Start</u>	<u>NT Stop</u>
RXA01382	GR00395	1397	
RXA01364	GR00396	4	
RXA01368	GR00397	980	
RXA01370	GR00398	2225	
RXA01372	GR00399	1	591
RXA01379	GR00402	6	
RXA01398	GR00408	8475	6218
RXA01397	GR00408	1369	
RXA01409	GR00410	6894	6475
RXA01428	GR00417	5298	4481
RXA01439	GR00418	5651	6268
RXA01467	GR00421	5949	6494
RXA01505	GR00424	2493	1330
RXA01523	GR00424	2179	1349
RXA01497	GR00424	262	1179
RXA01901	GR00424	8130	7943
RXA01905	GR00424	11318	11815
RXA01753	GR00424	27951	28901
RXA01995	GR00447	3328	4285
RXA01900	GR00447	10460	11128
RXA01672	GR00452	1908	2510
RXA01662	GR00462	1090	2432
RXA01709	GR00483	745	416
RXA01715	GR00485	1267	1962
RXA01718	GR00491	3971	4884
RXA01803	GR00509	5671	4712
RXA01804	GR00509	8117	5797
RXA01805	GR00509	8515	6186
RXA01844	GR00522	1950	1771
RXA01871	GR00534	2797	3759
RXA01875	GR00536	516	1313
RXA01877	GR00537	135	1199
RXA01879	GR00537	2117	2104
RXA01880	GR00537	2641	3048
RXA01898	GR00544	2	580
RXA01916	GR00549	1034	2044
RXA01931	GR00555	4913	6586
RXA01942	GR00557	3526	2927
RXA01992	GR00581	709	280
RXA02023	GR00613	3234	4001
RXA02057	GR00625	2972	3502
RXA02071	GR00628	458	6
RXA02104	GR00631	5327	4908
RXA02108	GR00632	2077	2511
RXA02117	GR00636	1056	1529
RXA02121	GR00636	6558	7928
RXA02124	GR00636	7956	9911
RXA02166	GR00640	13048	13224
RXA02177	GR00641	12683	13615
RXA02167	GR00641	21249	23447
RXA02211	GR00648	2537	2989

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<u>Identification Code</u>	<u>NT Config.</u>	<u>NT Start</u>	<u>NT Stop</u>
RXA02216	CR00851	2	107
RXA02217	CR00851	968	306
RXA02218	CR00851	1299	1565
RXA02219	CR00851	1578	2983
RXA02255	CR00854	22507	23442
RXA02298	CR00862	10310	8652
RXA02308	CR00864	939	511
RXA02337	CR00872	2891	3816
RXA02347	CR00877	509	189
RXA02349	CR00878	394	5
RXA02352	CR00881	2	556
RXA02387	CR00894	683	6
RXA02393	CR00897	168	449
RXA02395	CR00898	2	733
RXA02198	CR00698	1309	1031
RXA02407	CR00701	1580	1885
RXA02409	CR00702	1248	835
RXA02430	CR00707	7498	7683
RXA02459	CR00712	4341	5075
RXA02472	CR00715	5435	5725
RXA02484	CR00718	2317	1817
RXA02486	CR00718	3441	4076
RXA02498	CR00720	10025	9219
RXA02514	CR00723	1	837
RXA02518	CR00723	3484	3874
RXA02521	CR00724	2924	4166
RXA02525	CR00725	3113	3490
RXA02540	CR00726	12438	12001
RXA02601	CR00742	5258	7246
RXA02617	CR00745	1404	1910
RXA02639	CR00749	511	1344
RXA02672	CR00753	12303	13400
RXA02714	CR00758	14754	14326
RXA02720	CR00759	631	5
RXA02751	CR00764	6193	5920
RXA02768	CR00770	986	594
RXA02789	CR00777	5237	5762
RXA02798	CR00778	1648	1100
RXA02874	CR00115	1348	889
RXA02891	CR10040	9518	10195
RXA01504	CR00424	10710	11318
RXA01506	CR00424	11615	12225
RXA01647	CR00456	12422	11535
RXA01798	CR00508	2	484
RXA02132	CR00638	737	1375
RXA02254	CR00654	21769	22449
RXA02482	CR00718	914	105
RXA02789	CR00780	182	454
RXA00052	CR00008	7957	7247

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<u>Identification</u>	<u>Code</u>	<u>Canig.</u>	<u>Start</u>	<u>NT</u>	<u>NT</u>	<u>Stop</u>
RXA00160	GR00028	2334	1795			
RXA00161	GR00204	1384	2168			
RXA00162	GR00253	486	104			
RXA01213	GR00367	28475	25042			
RXA02798	GR00776	2842	4286			
RXA02847	GR00847	598	5			
RXA02898	CR10040	1651	6			
RXA02899	QR10040	2125	1846			
RXA00075	CR00013	2211	3647			
RXA00093	CR00014	204	2428			
RXA00101	CR00014	10514	10107			
RXA00108	CR00015	546	4			
RXA00197	CR00030	1731	2741			
RXA00297	CR00048	2861	3772			
RXA00301	CR00049	1970	2506			
RXA00336	CR00057	19461	19931			
RXA00044	CR00063	6	584			
RXA00418	CR00093	1	327			
RXA00418	GR00094	1	1085			
RXA00430	GR00098	3473	3083			
RXA00447	CR00108	518	817			
RXA00455	CR00113	2	619			
RXA00485	GR00119	25230	23188			
RXA00490	GR00121	2876	1774			
RXA00508	CR00126	489	1829			
RXA00515	CR00131	3	482			
RXA00520	CR00132	599	796			
RXA00602	CR00159	4907	4155			
RXA00611	CR00161	3640	2165			
RXA00688	CR00176	797	6			
RXA00674	CR00177	755	6			
RXA00731	CR00195	2613	142			
RXA00830	GR00224	266	988			
RXA00835	GR00228	3	692			
RXA01088	GR00298	2184	3254			
RXA01071	QR00289	2822	2438			
RXA01102	GR00306	10018	8774			
RXA01119	GR00310	1068	119			
RXA01158	GR00328	2580	1639			
RXA01177	GR00335	2121	4108			
RXA01229	GR00355	2806	3498			
RXA01331	GR00367	1608	1031			
RXA01507	GR00424	12339	12861			
RXA01623	GR00452	2514	3224			
RXA01624	GR00452	3220	3564			
RXA01669	GR00465	1002	271			
RXA01673	GR00487	1807	773			
RXA01685	GR00470	1488	910			

<u>Identification</u>	<u>Code</u>	<u>Config.</u>	<u>NT</u>	<u>NT</u>
			<u>Start</u>	<u>Stop</u>
RXA011749	GR00495	GR00495	4633	6249
RXA01886	GR00509	GR00509	6595	7074
RXA02080	GR00628	GR00628	11017	10211
RXA02172	GR00841	GR00841	8919	8581
RXA02295	GR00862	GR00862	8842	6063
RXA02297	GR00862	GR00862	7502	8638
RXA02390	GR00695	GR00695	1500	812
RXA02408	GR00702	GR00702	812	5
RXA02448	GR00719	GR00719	1	369
RXA02449	GR00719	GR00719	373	996
RXA02455	GR00720	GR00720	9002	6435
RXA02524	GR00725	GR00725	2405	3084
RXA02544	GR00728	GR00728	16715	18142
RXA02584	GR00741	GR00741	8875	8515
RXA02635	GR00741	GR00741	9917	0937
RXA02638	GR00742	GR00742	2516	3166
RXA02680	GR00742	GR00742	5027	3830
RXA02692	GR00742	GR00742	7239	7742
RXA02694	GR00742	GR00742	18800	10875
RXA02693	GR00755	GR00755	1650	4
RXA02700	GR00757	GR00757	3507	4742
RXA02701	GR00757	GR00757	4838	6145
RXA02654	GR00169	GR00169	7213	8478
RXA01425	GR00417	GR00417	1701	2585
RXA02549	GR00728	GR00728	1331	6
RXA02619	GR00740	GR00740	4365	3918
RXA02580	GR00740	GR00740	4982	4219
RXA00808	GR00216	GR00216	2177	5
RXA00808	GR00217	GR00217	1029	352
RXA01318	GR00382	GR00382	3616	2315
RXA01677	GR00467	GR00467	5043	4300
RXA01688	GR00461	GR00461	5	1469
RXA02697	GR00757	GR00757	1	699
RXA02719	GR00758	GR00758	19598	20245
RXA00003	GR00001	GR00001	2279	3019
RXA00015	GR00002	GR00002	5899	6307
RXA00016	GR00002	GR00002	12978	14277
RXA00020	GR00002	GR00002	17142	16363
RXA00021	GR00002	GR00002	18766	20518
RXA00022	GR00002	GR00002	20583	21297
RXA00028	GR00003	GR00003	8058	6112
RXA00031	GR00003	GR00003	10383	9982
RXA00036	GR00004	GR00004	7204	8619
RXA00037	GR00004	GR00004	9557	8685
RXA00039	GR00006	GR00006	2089	1451
RXA00040	GR00006	GR00006	2499	2095

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<u>Identification</u>	<u>Code</u>	<u>Config.</u>	<u>Start</u>	<u>NT</u>	<u>Stop</u>
RXA00047	CR00008	514	95	2956	
RXA00049	GR00008	2270			
RXA00058	GR00009	1463	714		
RXA00059	CR00009	7394	6831		
RXA00059	CR00009	8301	8020		
RXA00083	CR00010	1658	1374		
RXA00085	CR00010	4140	4412		
RXA00087	CR00011	708	223		
RXA00088	CR00011	1305	724		
RXA00077	CR00012	4228	5589		
RXA00079	CR00012	8599	6820		
RXA00080	CR00012	7342	6923		
RXA00082	CR00012	9019	8456		
RXA00083	CR00013	771	1070		
RXA00088	CR00013	2739	3092		
RXA00087	QR00013	3983	3456		
RXA00094	CR00014	3163	3435		
RXA00110	CR00016	364	912		
RXA00114	CR00017	3420	3908		
RXA00119	CR00019	1704	2462		
RXA00120	GR00019	2798	3451		
RXA00121	CR00019	3473	4183		
RXA00127	GR00020	2871	2416		
RXA00128	GR00020	4709	3096		
RXA00140	GR00022	3841	3658		
RXA00141	CR00022	4307	3846		
RXA00142	CR00022	4776	4300		
RXA00151	GR00023	4958	5552		
RXA00154	QR00023	8568	7728		
RXA00155	GR00023	8615	9397		
RXA00162	CR00024	5438	5191		
RXA00167	CR00025	4324	4564		
RXA00168	GR00026	5222	3150		
RXA00170	GR00026	9914	8081		
RXA00171	GR00028	10316	10086		
RXA00173	GR00027	1716	1384		
RXA00174	CR00027	2079	1795		
RXA00175	CR00027	2732	2103		
RXA00176	GR00027	3475	3317		
RXA00179	GR00028	1714	1258		
RXA00194	CR00030	290	6		
RXA00199	CR00031	2172	754		
RXA00200	GR00031	2437	2335		
RXA00207	GR00032	8430	6147		
RXA00211	GR00032	10120	10782		
RXA00218	GR00032	18104	19243		
RXA00222	GR00032	21073	22218		
RXA00230	GR00034	748	27		

<u>Identification</u>	<u>Code</u>	<u>NT</u>	<u>Stop</u>
<u>Config</u>	<u>Start</u>	<u>NT</u>	<u>Stop</u>
RXA00232	GR00035	527	18
RXA00236	GR00036	3300	2575
RXA00237	GR00036	3668	4045
RXA00238	GR00038	4188	4554
RXA00240	GR00036	5342	5133
RXA00242	GR00036	7031	8233
RXA00244	GR00037	1585	930
RXA00245	GR00037	2049	1565
RXA00250	GR00038	6	221
RXA00252	GR00038	485	727
RXA00255	GR00039	2	604
RXA00258	GR00039	988	1738
RXA00257	GR00039	1760	2215
RXA00258	GR00039	3219	3890
RXA00260	GR00039	9234	10408
RXA00261	GR00039	11693	11265
RXA00264	GR00040	2459	2836
RXA00267	GR00040	4091	3822
RXA00272	GR00041	4420	4791
RXA00273	GR00042	185	1297
RXA00274	GR00042	1556	4165
RXA00275	GR00042	4696	4238
RXA00276	GR00042	5016	4875
RXA00282	GR00044	793	5
RXA00283	GR00045	142	1269
RXA00286	GR00046	578	1142
RXA00294	GR00047	2781	3189
RXA00302	GR00049	2595	3416
RXA00303	GR00050	459	4
RXA00308	GR00052	1081	887
RXA00320	GR00057	358	537
RXA00326	GR00057	9378	9857
RXA00334	GR00057	16762	17097
RXA00337	GR00058	530	6
RXA00342	GR00061	73	501
RXA00371	GR00011	4013	5484
RXA00353	GR00068	988	1680
RXA00355	GR00069	635	510
RXA00357	GR00070	724	2768
RXA00358	GR00070	4069	5199
RXA00362	GR00073	2	961
RXA00373	GR00079	142	4
RXA00375	GR00080	549	49
RXA00380	GR00082	838	216
RXA00384	GR00083	395	6
RXA00387	GR00084	1403	591
RXA00390	GR00086	1437	1841
RXA00392	GR00086	3890	3027

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<u>Identification</u>	<u>Code</u>	<u>NT</u>	<u>NT</u>	<u>Stop</u>
	<u>Contig.</u>	<u>Start</u>		
RXA00394	GR00086	5322	4990	
RXA00395	GR00086	5417	5716	
RXA00397	GR00086	7208	6667	
RXA00398	GR00087	1	681	
RXA00408	GR00091	842	1088	
RXA00409	GR00091	1088	2500	
RXA00423	GR00097	809	457	
RXA00424	GR00097	1379	909	
RXA00425	GR00097	1433	1857	
RXA00429	GR00098	2053	2682	
RXA00431	GR00100	1448	1970	
RXA00451	GR00110	816	325	
RXA00457	GR00114	1451	372	
RXA00463	GR00116	4209	3388	
RXA00468	GR00118	1282	464	
RXA00469	GR00119	1647	472	
RXA00472	GR00119	5449	4589	
RXA00475	GR00119	8822	8163	
RXA00476	GR00119	8961	9821	
RXA00481	GR00119	17636	18220	
RXA00486	GR00120	1	702	
RXA00493	GR00123	3	228	
RXA00498	GR00123	1776	2177	
RXA00504	GR00125	5007	5752	
RXA00507	GR00127	1098	244	
RXA00509	GR00128	316	140	
RXA00510	GR00128	384	914	
RXA00519	GR00132	4	516	
RXA00522	GR00134	111	575	
RXA00527	GR00136	3123	1380	
RXA00528	GR00136	3562	4650	
RXA00529	GR00136	5274	4732	
RXA00530	GR00136	6637	5537	
RXA00535	GR00137	5155	5811	
RXA00546	GR00142	1	690	
RXA00547	GR00142	841	1054	
RXA00548	GR00143	3	504	
RXA00549	GR00143	502	897	
RXA00550	GR00143	935	1255	
RXA00554	GR00145	1608	1138	
RXA00563	GR00151	1	2739	
RXA00564	GR00151	3744	4148	
RXA00568	GR00156	2916	2246	
RXA00577	GR00156	2980	3327	
RXA00582	GR00156	9442	8924	
RXA00585	GR00156	11884	11577	
RXA00589	GR00156	14220	14582	
RXA00595	GR00159	3	332	

<u>Identification Code</u>	<u>Config</u>	<u>Start</u>	<u>NT</u>	<u>Stop</u>	<u>NT</u>
RXA00597	GRO0159	797	1086	1387	1387
RXA00598	GRO0159	1070	3439	3749	3749
RXA00601	GRO0159	3439	5489	5779	5779
RXA00604	GRO0159	5489	5774	5918	5918
RXA00616	GRO0162	3574	4002	5084	5084
RXA00617	GRO0162	4002	172	1626	1626
RXA00631	GRO0166	172	446	6	6
RXA00646	GRO0169	446	1213	1213	1213
RXA00647	GRO0169	641	5997	5997	5997
RXA00652	GRO0169	5449	6160	6160	6160
RXA00653	GRO0169	6924	9235	9235	9235
RXA00656	GRO0169	9495	1153	1153	1153
RXA00661	GRO0172	684	1403	1403	1403
RXA00662	GRO0172	2871	3219	3219	3219
RXA00664	GRO0172	635	1393	1393	1393
RXA00676	GRO0173	647	103	103	103
RXA00678	GRO0173	1037	2317	2317	2317
RXA00679	GRO0179	3450	3921	3921	3921
RXA00681	GRO0181	4303	801	801	801
RXA00682	GRO0181	427	1348	1348	1348
RXA00683	GRO0182	2972	1348	1348	1348
RXA00701	GRO0183	377	500	500	500
RXA00704	GRO0185	1048	1249	1249	1249
RXA00707	GRO0187	1809	7000	7000	7000
RXA00712	GRO0188	7865	5	5	5
RXA00714	GRO0188	381	4	4	4
RXA00720	GRO0189	537	164	164	164
RXA00721	GRO0190	811	808	808	808
RXA00723	GRO0191	458	1068	1068	1068
RXA00724	GRO0191	1646	2054	2054	2054
RXA00725	GRO0192	841	701	701	701
RXA00726	GRO0192	642	642	642	642
RXA00728	GRO0194	1063	711	711	711
RXA00729	GRO0194	537	4	4	4
RXA00730	GRO0202	819	1375	1375	1375
RXA00739	GRO0202	1646	15654	15654	15654
RXA00740	GRO0202	2986	3888	3888	3888
RXA00741	GRO0202	5517	6230	6230	6230
RXA00742	GRO0202	6652	13341	13341	13341
RXA00743	GRO0202	13814	14945	14945	14945
RXA00745	GRO0202	13755	15087	15087	15087
RXA00746	GRO0202	15087	15360	15360	15360
RXA00747	GRO0202	15917	16542	16542	16542
RXA00748	GRO0202	17240	19374	19374	19374
RXA00749	GRO0202	18937	19418	19418	19418
RXA00750	GRO0202	20245	21419	21419	21419
RXA00751	GRO0202	21847	664	664	664
RXA00752	GRO0203	344	4372	4372	4372
RXA00754	GRO0203	3119	6838	6838	6838
RXA00757	GRO0204	6624			
RXA00169					

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<u>Identification Code</u>	<u>Config.</u>	<u>Start</u>	<u>NT</u>	<u>Stop</u>
RXA00771	GR00205	857	180	
RXA00785	GR00207	625	5	
RXA00788	GR00209	910	686	
RXA00795	GR00211	4228	4755	
RXA00804	GR00215	438	881	
RXA00811	GR00218	1695	2198	
RXA00812	GR00219	287	1345	
RXA00814	GR00219	2463	3236	
RXA00815	GR00219	3236	3808	
RXA00816	GR00219	4182	4878	
RXA00826	GR00221	567	37	
RXA00831	GR00224	1662	961	
RXA00838	GR00226	797	2487	
RXA00837	GR00227	540	247	
RXA00840	GR00228	742	1455	
RXA00841	GR00228	1486	2002	
RXA00853	GR00231	3775	3173	
RXA00854	GR00231	4708	4920	
RXA00855	GR00232	526	242	
RXA00862	GR00236	580	17	
RXA00876	GR00241	4208	2454	
RXA00881	GR00242	8057	8434	
RXA00882	GR00242	8788	9485	
RXA00883	GR00242	16080	9542	
RXA00893	GR00244	789	193	
RXA00895	GR00244	2578	1988	
RXA00904	GR00246	1457	702	
RXA00908	GR00247	1611	2168	
RXA00914	GR00250	1271	6	
RXA00915	GR00251	514	5	
RXA00916	GR00251	4108	518	
RXA00917	GR00251	5534	4152	
RXA00919	GR00252	1690	682	
RXA00920	GR00252	2852	1890	
RXA00921	GR00252	4750	2852	
RXA00922	GR00252	6409	4823	
RXA00923	GR00252	8857	6684	
RXA00924	GR00252	7278	6817	
RXA00925	GR00252	8546	7281	
RXA00932	GR00253	5088	5541	
RXA00933	GR00253	8047	5596	
RXA00943	GR00258	3	509	
RXA00946	GR00259	1034	3807	
RXA00959	GR00285	402	728	
RXA00963	GR00289	442	5	
RXA00969	GR00273	1	147	
RXA00971	GR00273	1421	1149	
RXA00973	GR00274	2272	1670	

<u>Identification</u>	<u>Code</u>	<u>NT</u>	<u>Start</u>	<u>Stop</u>
RXA00978	GR00276	217	831	949
RXA00988	GR00280	1311	1165	1165
RXA01005	GR00286	520	866	866
RXA01007	GR00287	2572	4859	4859
RXA01008	GR00287	2719	494	494
RXA01016	GR00289	1141	626	626
RXA01028	GR00295	3	1338	1826
RXA01029	GR00295	1182	3847	3847
RXA01031	GR00295	3974	4348	4348
RXA01032	GR00295	4353	4698	4698
RXA01033	GR00295	5177	4824	4824
RXA01034	GR00295	5818	8423	8423
RXA01035	GR00295	6513	6985	6985
RXA01036	GR00295	7000	7527	7527
RXA01037	GR00295	7530	8276	8276
RXA01038	GR00295	9540	10613	10613
RXA01039	GR00295	9711	10932	10932
RXA01040	GR00295	10780	12385	12385
RXA01041	GR00295	11088	13446	13446
RXA01042	GR00295	12774	15280	15280
RXA01043	GR00295	14024	17230	17230
RXA01044	GR00295	15407	19219	19219
RXA01045	GR00295	17441	19717	19717
RXA01046	GR00295	19244	8246	8246
RXA01047	GR00296	8568	5	5
RXA01058	GR00297	490	489	489
RXA01062	GR00297	828	1330	1330
RXA01063	GR00297	605	4	4
RXA01066	GR00299	606	2859	2859
RXA01069	GR00300	3269	1502	1502
RXA01075	GR00302	1777	4	4
RXA01083	GR00303	980	463	463
RXA01085	GR00304	2	861	861
RXA01086	GR00305	702	1092	1092
RXA01087	GR00306	4341	10992	10992
RXA01098	GR00306	10316	14811	14811
RXA01103	GR00306	13612	14912	14912
RXA01107	GR00306	15582	15640	15640
RXA01108	GR00306	16281	870	870
RXA01109	GR00307	1	3156	3156
RXA01112	GR00310	2479	36	36
RXA01121	GR00311	557	844	844
RXA01122	GR00311	1090	280	280
RXA01123	GR00311	2	312	312
RXA01127	GR00314	1125	1311	1311
RXA01128	GR00315	445	460	460
RXA01131	GR00317			
RXA01134				

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<u>Identification</u>	<u>Code</u>	<u>Config.</u>	<u>NT</u>	<u>Stop</u>
			<u>Start</u>	<u>NT</u>
RXA01197	CR00J18	1101	1480	
RXA01140	CR00J18	3272	4057	
RXA01148	CR00J23	1452	2051	
RXA01153	CR00J25	546	4	
RXA01154	CR00J26	808	6	
RXA01155	CR00J27	1370	6	
RXA01150	CR00J27	1588	1388	
RXA01160	CR00J28	4187	3213	
RXA01163	CR00J31	710	6	
RXA01165	CR00J32	2155	1583	
RXA01168	CR00J32	3005	2523	
RXA01167	CR00J33	3	323	
RXA01169	CR00J34	1	567	
RXA01170	CR00J34	838	1120	
RXA01171	CR00J34	1714	2406	
RXA01173	CR00J34	4853	4239	
RXA01174	CR00J34	6004	5255	
RXA01176	CR00J35	4106	4555	
RXA01184	CR00J38	1489	17	
RXA01187	CR00J38	3850	4308	
RXA01206	CR00J46	593	853	
RXA01210	CR00J49	3	695	
RXA01213	CR00J51	1508	282	
RXA01218	CR00J53	1078	1505	
RXA01221	CR00J56	1384	1887	
RXA01233	CR00J56	4242	3871	
RXA01244	CR00J57	633	250	
RXA01256	CR00J65	5613	5785	
RXA01283	CR00J67	10720	11631	
RXA01287	CR00J67	16799	15488	
RXA01275	CR00J67	28418	29335	
RXA01276	CR00J67	29883	30539	
RXA01281	CR00J89	3869	4630	
RXA01295	CR00J73	3764	4738	
RXA01298	CR00J73	5836	4754	
RXA01301	CR00J75	1993	1589	
RXA01104	CR00J76	1982	2467	
RXA01308	CR00J76	5691	4684	
RXA01110	CR00J80	803	477	
RXA01113	CR00J81	1116	172	
RXA01115	CR00J82	1394	744	
RXA01116	CR00J82	1855	1563	
RXA01117	CR00J82	2296	1877	
RXA01126	CR00J86	45	338	
RXA01330	CR00J87	569	1024	
RXA01331	CR00J89	1231	227	
RXA01338	CR00J89	1640	1038	
RXA01337	CR00J89	5005	3653	

<u>Identification</u>	<u>NT</u>	<u>NT</u>
<u>Code</u>	<u>Start</u>	<u>Stop</u>
	<u>Config:</u>	
RXA01349	GR00392	1531
RXA01378	GR00401	1281
RXA01380	GR00408	1147
RXA01384	GR00406	3238
RXA01380	GR00408	992
RXA01391	GR00408	2078
RXA01400	GR00409	2988
RXA01401	GR00409	3193
RXA01402	GR00409	3508
RXA01403	GR00409	4410
RXA01405	GR00410	1844
RXA01410	GR00411	686
RXA01413	GR00412	854
RXA01414	GR00412	1628
RXA01415	GR00412	2192
RXA01417	GR00414	845
RXA01421	GR00416	1215
RXA01422	GR00416	2003
RXA01424	GR00417	10228
RXA01440	GR00418	7498
RXA01441	GR00418	8542
RXA01445	GR00418	15081
RXA01447	GR00418	17885
RXA01448	GR00418	18796
RXA01452	GR00419	2363
RXA01456	GR00420	898
RXA01457	GR00420	1499
RXA01459	GR00420	3311
RXA01460	GR00420	4068
RXA01469	GR00422	2091
RXA01470	GR00422	4112
RXA01471	GR00422	5243
RXA01472	GR00422	5783
RXA01473	GR00422	6596
RXA01474	GR00422	6878
RXA01475	GR00422	7651
RXA01478	GR00422	7847
RXA01479	GR00422	12423
RXA01484	GR00422	20688
RXA01485	GR00422	20230
RXA01516	GR00424	21228
RXA01519	GR00424	23725
RXA01520	GR00424	24784
RXA01525	GR00424	32301
RXA01527	GR00425	5126
RXA01529	GR00426	2
RXA01536	GR00427	4086
RXA01538	GR00428	120

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<u>Identification</u>	<u>NT</u>	<u>Stop</u>
<u>Code</u>	<u>Config</u>	<u>Start</u>
RXA01540	CR00428	3081
RXA01542	GR00429	3
RXA01543	GR00430	5063
RXA01544	GR00430	2802
RXA01545	GR00440	3498
RXA01546	CR00440	4838
RXA01547	GR00440	5284
RXA01548	GR00440	6371
RXA01549	GR00440	7432
RXA01550	GR00440	8428
RXA01552	GR00441	8428
RXA01554	GR00442	7119
RXA01557	GR00443	959
RXA01560	GR00445	767
RXA01563	GR00447	1176
RXA01566	GR00447	1668
RXA01567	GR00447	2213
RXA01574	GR00448	6963
RXA01575	GR00448	8024
RXA01579	GR00449	671
RXA01586	GR00449	1597
RXA01587	GR00442	120
RXA01590	GR00445	1710
RXA01598	GR00447	7414
RXA01602	GR00447	13591
RXA01605	GR00448	860
RXA01610	GR00449	4343
RXA01611	GR00449	4832
RXA01612	GR00449	5235
RXA01618	GR00451	1387
RXA01619	GR00451	2407
RXA01627	GR00453	1
RXA01628	CR00451	495
RXA01630	GR00454	866
RXA01634	GR00454	341
RXA01638	GR00456	4988
RXA01639	GR00456	825
RXA01639	GR00456	1334
RXA01641	GR00456	5182
RXA01642	GR00458	6557
RXA01643	GR00458	8374
RXA01652	GR00458	971
RXA01659	GR00462	6
RXA01663	GR00463	486
RXA01665	GR00463	4
RXA01666	GR00463	438
RXA01672	GR00467	2152
RXA01675	GR00467	2
RXA01676	CR00467	2624
RXA01681	GR00467	4179
RXA01684	GR00470	10681
RXA01688	GR00470	2026

<u>Identification Code</u>	<u>Config</u>	<u>NT Start</u>	<u>NT Stop</u>
RXA01694	GR00474	3931	3032
RXA01697	GR00476	761	1488
RXA01701	GR00476	196	528
RXA01703	GR00479	2118	1648
RXA01708	GR00482	312	602
RXA01711	GR00484	2007	850
RXA01714	GR00485	985	371
RXA01729	GR00489	2636	3154
RXA01731	GR00491	109	807
RXA01734	GR00492	544	1077
RXA01741	GR00493	7535	6738
RXA01742	GR00493	7614	8117
RXA01750	GR00496	1878	3518
RXA01751	GR00496	5576	5830
RXA01752	GR00497	557	6
RXA01753	GR00497	2095	557
RXA01754	GR00497	4082	2142
RXA01760	GR00498	5095	5316
RXA01761	GR00499	7001	5484
RXA01765	GR00500	3144	4085
RXA01767	GR00501	341	6
RXA01768	GR00501	827	450
RXA01769	GR00501	1275	847
RXA01770	GR00501	5134	1370
RXA01771	GR00502	886	185
RXA01773	GR00503	34	444
RXA01774	GR00503	634	1416
RXA01775	GR00504	178	741
RXA01776	GR00504	838	2289
RXA01777	GR00504	2319	2777
RXA01778	GR00504	2912	4048
RXA01779	GR00504	4246	5684
RXA01780	GR00504	5721	6095
RXA01781	GR00504	6052	6312
RXA01782	GR00504	6384	6779
RXA01783	GR00504	6842	7078
RXA01785	GR00505	729	1304
RXA01787	GR00506	2	355
RXA01788	GR00506	381	801
RXA01789	GR00506	875	1516
RXA01790	GR00506	1672	1731
RXA01791	GR00506	1885	2247
RXA01792	GR00508	2310	2582
RXA01793	GR00508	2916	3149
RXA01794	GR00506	3194	3427
RXA01799	GR00509	377	1570
RXA01800	GR00509	2292	1573
RXA01809	GR00510	3	638

<u>Identification</u>	<u>Code</u>	<u>Confg</u>	<u>Start</u>	<u>NT</u>	<u>Stop</u>
RXA01812		GR00514	3	1232	
RXA01813		GR00515	635	6	
RXA01816		GR00515	4210	4941	
RXA01817		GR00515	4941	5573	
RXA01820		GR00515	8380	9733	
RXA01825		GR00516	2847	2578	
RXA01831		GR00516	10874	10413	
RXA01834		GR00517	2478	1777	
RXA01832		GR00522	1397	480	
RXA01843		GR00522	876	1067	
RXA01845		GR00522	1919	2126	
RXA01846		GR00523	261	4	
RXA01847		GR00524	52	786	
RXA01844		GR00525	5892	5946	
RXA01835		GR00526	1	1816	
RXA01838		GR00527	225	770	
RXA01857		GR00527	939	1589	
RXA01858		GR00529	679	6	
RXA01870		GR00534	2123	2797	
RXA01874		GR00535	2556	2803	
RXA01899		GR00544	1874	2859	
RXA01902		GR00544	7957	7094	
RXA01903		GR00545	3	281	
RXA01904		GR00545	762	340	
RXA01905		GR00545	1074	1604	
RXA01906		GR00545	2322	2786	
RXA01907		GR00545	3176	3787	
RXA01908		GR00545	4030	4512	
RXA01909		GR00546	59	937	
RXA01910		GR00546	1030	1875	
RXA01911		GR00546	2199	3044	
RXA01921		GR00551	943	5	
RXA01923		GR00552	1311	1719	
RXA01924		GR00553	1	837	
RXA01925		GR00553	1008	1674	
RXA01910		GR00555	3817	2807	
RXA01941		GR00557	995	1429	
RXA01956		GR00563	221	1270	
RXA01957		GR00564	389	850	
RXA01958		GR00564	910	1416	
RXA01959		GR00584	1639	2019	
RXA01980		GR00585	187	504	
RXA01981		GR00585	521	1000	
RXA01982		GR00585	1022	1591	
RXA01983		GR00585	1757	2440	
RXA01984		GR00586	1329	4	
RXA01985		GR00586	1935	1375	
RXA01989		GR00587	5889	5216	

<u>Identification</u>	<u>Code</u>	<u>Config.</u>	<u>NT Start</u>	<u>NT Stop</u>
RXA01973	GR00570	2	583	
RXA01974	GR00570	658	2109	
RXA01976	GR00571	3742	2222	
RXA01977	GR00571	4647	3972	
RXA01978	GR00572	1	1187	
RXA01981	GR00573	2105	2563	
RXA01987	GR00576	167	379	
RXA01988	GR00576	779	462	
RXA01990	GR00581	1	999	
RXA01991	GR00581	928	1720	
RXA01999	GR00589	2384	2854	
RXA02001	GR00590	700	152	
RXA02003	GR00593	601	4	
RXA02004	GR00594	3	200	
RXA02005	GR00594	168	447	
RXA02006	GR00597	498	4	
RXA02007	GR00598	651	223	
RXA02009	GR00601	127	5	
RXA02011	GR00603	48	363	
RXA02013	GR00607	553	5	
RXA02014	GR00607	915	540	
RXA02019	GR00612	597	106	
RXA02021	GR00613	2008	1061	
RXA02036	GR00619	3441	3821	
RXA02039	GR00621	3	812	
RXA02040	GR00621	1452	925	
RXA02045	GR00623	1913	2173	
RXA02046	GR00623	2680	2843	
RXA02049	GR00624	1583	2029	
RXA02050	GR00624	2462	2833	
RXA02051	GR00624	3168	1683	
RXA02053	GR00624	5484	6062	
RXA02058	GR00635	4051	3500	
RXA02059	GR00635	4878	4184	
RXA02066	GR00626	6187	6678	
RXA02087	GR00626	6713	7188	
RXA02089	GR00627	1116	1694	
RXA02081	GR00628	12307	13935	
RXA02084	GR00629	2920	2576	
RXA02089	GR00629	8431	8901	
RXA02090	GR00629	9764	8984	
RXA02091	GR00639	10512	8862	
RXA02094	GR00639	13282	13998	
RXA02097	GR00630	184	1555	
RXA02102	GR00631	4479	3322	
RXA02103	GR00631	4510	4905	
RXA02109	GR00632	3480	2540	
RXA02114	GR00634	6115	130	

<u>Identification</u>	<u>NT</u>	<u>Stop</u>
<u>Code</u>	<u>Start</u>	
<u>Config.</u>		
RXA02121	GR00636	5813
RXA02125	GR00637	739
RXA02129	GR00637	5906
RXA02146	GR00639	14742
RXA02151	GR00639	19813
RXA02152	GR00640	237
RXA02163	GR00640	10072
RXA02164	GR00640	10824
RXA02165	GR00640	12398
RXA02168	GR00641	12388
RXA02169	GR00641	2894
RXA02170	GR00641	3172
RXA02178	GR00641	4798
RXA02181	GR00641	13628
RXA02185	GR00641	17168
RXA02186	GR00641	20185
RXA02187	GR00641	21213
RXA02199	GR00646	2591
RXA02203	GR00646	7469
RXA02208	GR00648	9827
RXA02207	GR00646	10909
RXA02212	GR00649	964
RXA02221	GR00651	6720
RXA02226	GR00651	8081
RXA02227	GR00651	1059
RXA02230	GR00651	1236
RXA02231	GR00651	4158
RXA02238	GR00651	5111
RXA02268	GR00654	5241
RXA02267	GR00655	653
RXA02271	GR00655	2053
RXA02279	GR00657	5406
RXA02280	GR00658	1
RXA02281	GR00660	2
RXA02285	GR00660	532
RXA02286	GR00660	1544
RXA02287	GR00660	3285
RXA02287	GR00660	4071
RXA02294	GR00662	5992
RXA02298	GR00662	6978
RXA02300	GR00662	11184
RXA02301	GR00662	11910
RXA02302	GR00662	12036
RXA02303	GR00663	1
RXA02304	GR00663	1613
RXA02307	GR00664	395
RXA02325	GR00668	4114
RXA02330	GR00670	605
RXA02331	GR00671	396
RXA02336	GR00672	2731

Table I, Page 21

<u>Identification Code</u>	<u>Config.</u>	<u>NT Start</u>	<u>Stop</u>
RXA02339	GR00873	484	5
RXA02339	GR00874		492
RXA02340	GR00874	1214	576
RXA02341	GR00875	415	5
RXA02356	GR00884	761	1756
RXA02358	GR00885	1239	1529
RXA02360	GR00885	3644	6076
RXA02381	GR00885	6160	6810
RXA02382	GR00885	7045	10743
RXA02386	GR00887	254	1581
RXA02388	GR00887	2918	2244
RXA02394	GR00888	1626	2246
RXA02391	GR00891	1792	770
RXA02390	GR00898	2841	4370
RXA02401	GR00899	1191	4491
RXA02406	GR00701	1322	774
RXA02412	GR00703	2043	2522
RXA02415	GR00704	655	170
RXA02417	GR00705	4755	2632
RXA02421	GR00705	7237	6428
RXA02423	GR00708	221	6
RXA02428	GR00707	4585	3452
RXA02433	GR00708	2981	3580
RXA02437	GR00709	1661	2470
RXA02444	GR00709	7818	9113
RXA02454	GR00711	3	815
RXA02457	GR00712	1285	2404
RXA02480	GR00712	5839	5318
RXA02481	GR00712	6252	5845
RXA02484	GR00713	1107	1613
RXA02485	GR00713	2014	1616
RXA02486	GR00714	92	6
RXA02487	GR00714	643	419
RXA02473	GR00715	6864	5924
RXA02475	GR00715	9585	8441
RXA02478	GR00716	1245	10
RXA02483	GR00718	1813	1001
RXA02498	GR00720	11016	11819
RXA02500	GR00720	14480	13558
RXA02505	GR00720	18423	18593
RXA02508	GR00720	19484	18603
RXA02510	GR00721	1983	2616
RXA02519	GR00724	1913	128
RXA02520	GR00724	2222	2905
RXA02534	GR00728	5536	6339
RXA02537	GR00728	8961	9422
RXA02538	GR00728	9422	10093
RXA02546	GR00728	19927	18824

<u>Identification</u>	<u>Code</u>	<u>Config.</u>	<u>Start</u>	<u>NT</u>	<u>Stop</u>
RXA02552		GR00730	924	110	
RXA02554		GR00731	1050	427	
RXA02555		GR00731	1757	1155	
RXA02556		GR00732	2543	3217	
RXA02558		GR00735	1363	5	
RXA02569		GR00736	82	831	
RXA02570		GR00736	837	1478	
RXA02576		GR00740	1569	148	
RXA02584		GR00740	19077	18754	
RXA02588		GR00740	2463	1579	
RXA02591		GR00741	15780	17609	
RXA02593		GR00741	18693	18481	
RXA02594		GR00741	19077	18754	
RXA02606		GR00742	13514	12144	
RXA02609		GR00742	10197	16445	
RXA02610		GR00742	16452	17378	
RXA02619		GR00746	204	1103	
RXA02620		GR00746	1192	1845	
RXA02624		GR00746	5802	4889	
RXA02647		GR00751	4155	4616	
RXA02649		GR00752	1284	283	
RXA02652		GR00752	2973	3551	
RXA02655		GR00752	9313	8330	
RXA02682		GR00753	1461	1724	
RXA02670		GR00753	10189	10780	
RXA02673		GR00753	14030	13398	
RXA02676		GR00754	3868	4775	
RXA02679		GR00754	5268	5693	
RXA02680		GR00754	6392	5109	
RXA02681		GR00754	5751	6184	
RXA02683		GR00754	7742	7085	
RXA02685		GR00754	10058	9402	
RXA02686		GR00756	742	287	
RXA02712		GR00758	13087	12273	
RXA02715		GR00758	15847	15458	
RXA02725		GR00760	1478	887	
RXA02727		GR00780	6287	5376	
RXA02734		GR00762	6514	68897	
RXA02736		GR00763	1751	797	
RXA02744		GR00763	14480	13857	
RXA02753		GR00765	2630	138	
RXA02758		GR00766	3851	2981	
RXA02757		GR00766	4475	3930	
RXA02765		GR00769	3552	2794	
RXA02770		GR00772	3	1322	
RXA02774		GR00773	3	473	
RXA02775		GR00773	744	968	
RXA02776		GR00773	1711	1372	
RXA02777		GR00773	4628	5732	

<u>Identification Code</u>	<u>Config.</u>	<u>NT Start</u>	<u>NT Stop</u>
RXA02778	CR00773	10095	10319
RXA02779	CR00773	10617	10895
RXA02780	CR00773	10954	11280
RXA02781	CR00774	11245	1155
RXA02782	CR00775	204	875
RXA02783	CR00775	845	1393
RXA02784	CR00775	1751	1936
RXA02785	CR00777	2	808
RXA02793	CR00777	9365	8684
RXA02812	CR00793	2	568
RXA02815	CR00798	1	554
RXA02816	CR00797	2	499
RXA02817	CR00798	403	5
RXA02818	CR00799	611	6
RXA02823	CR00804	275	6
RXA02825	CR00806	565	182
RXA02827	CR00812	428	6
RXA02835	CR00824	289	523
RXA02838	CR00831	1	462
RXA02841	CR00840	283	5
RXA02842	CR00841	356	15
RXA02844	CR00843	247	495
RXA02845	CR00844	2	816
RXA02848	CR00845	578	6
RXA02856	CR10003	459	211
RXA02858	CR10004	1382	167
RXA02862	CR10008	1695	2330
RXA02867	CR10008	610	5
RXA02888	CR10008	2017	1262
RXA02889	CR10009	390	4
RXA02890	CR10011	6	344
RXA02891	CR10011	398	830
RXA02892	CR10016	405	1087
RXA02893	CR10019	94	759
RXA02894	CR10020	2	724
RXA02895	CR10021	1	1518
RXA02898	CR10024	328	754
RXA02899	CR10026	1121	2706
RXA02891	CR10035	1	802
RXA02892	CR10035	1171	668
RXA02898	CR10038	256	5
RXA02895	CR10044	417	4
RXA01494	CR00423	8515	7520
RXA01092	CR00305	702	881
RXA01186	CR00338	3742	2845

TABLE 2: GENES IDENTIFIED FROM GENBANK

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-amino acids using said strains," Patent: EP-0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydrogenase	Mockel, B. et al. "Production of L-isotucine by means of recombinant micro-organisms with deregulated threonine dehydrogenase," Patent, WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochim. Biophys. Res Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	disR		Kimura, E. et al. "Molecular cloning of a novel gene, disR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium laevifermatum</i> ," <i>Biochi Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	disR1; disR2	D-glutamate racemase	
AB020624	murJ	transketolase	
AB023377	tkI		
AB024708	gltB; gltD	Glutamic 2-oxoglutarate aminotransferase large and small subunits	
AB023424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; adenylyltransferase	
AF005242	argC	N-acetylglutamate- γ -semialdehyde dihydrogenase	
AF005635	glnA	Glutamine synthetase cyclase	
AF030405	hisF	L-argininosuccinate synthetase	
AF030520	argG	Ornithine carbamoyltransferase	
AF031518	argJ	1-dihydroquinol dehydrogenase	
AF036932	aroD		

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF038348	pvc	Pyruvate carboxylase Dipeptide-binding protein; adenosine phosphotriphosphotransferase; GTP pyrophosphokinase	Wehmeyer, L. et al. "The role of the <i>Corynebacterium glutamicum</i> <i>rel</i> gene in (P)ppGpp metabolism." <i>Microbiology</i> , 144, 1853-1862 (1998)
AF038651	dctA; E; nptI; rrJ	Arginine repressor	
AF041436	argR	Inositol monophosphate phosphatase	
AF045998	impA	Argininosuccinate lyase	
AF048764	argH	N-acetylglutamylphosphate reductase;	
AF049897	argC; argF; argH; argD; argE; argR; argG; argI	ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino- δ -amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	mclA	Homoserine O-acetyltransferase	Paik, S. et al. "Isolation and analysis of <i>mclA</i> , a methionine biosynthetic gene encoding homoserine acetyltransferase in <i>Corynebacterium glutamicum</i> ," <i>Mol Cells.</i> , 8(3):286-294 (1998)
AF053071	aroB	Dihydroquinate synthetase	
AF060558	histI	Glutamine amidotransferase	
AF086704	histE	Phosphoribosyl-ATP	
AF114233	aroA	Pyrophosphophydrolase	
AF116184	panD	S-enolpyruvylshikimate 3-phosphate synthase <i>L</i> -aspartate- α -ketoglutarate decarboxylase precursor	Dusch, N. et al. "Expression of the <i>Corynebacterium glutamicum</i> <i>panD</i> gene encoding L-aspartate- α -ketoglutarate decarboxylase leads to pantotheneic acid overproduction in <i>Escherichia coli</i> ," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)

Table 2, Page 2

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	aroD; aroE	3-dehydroquinas; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pcpQ	Chorismate synthase; shikimate kinase; 3-dehydroquinate synthase; putative cytoplasmic peptidase	
AF145897	inhA		Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes. Identification, sequencing, and characterization of the proline/leucine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EcP." <i>J Bacteriol.</i> 180(22):6015-6012 (1998).
AF145898	inhA		Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with Corynebacterium glutamicum." <i>J Bacteriol.</i> 180(12):3159-3165 (1998)
AJ001436	ecpP		
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	
AJ007732	ppc; secG; ami; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY; glnB; glnD; sfp; amtp	Involved in cell division; PII protein; uridylyltransferase (uridyl)-removing enzyme; signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins." <i>FEMS Microbiol.</i> 173(2):303-310 (1999)
AJ132968	cal	Chloramphenicol acetyl transferase	
AJ224946	nqo	L-malate: quinone oxidoreductase	Molenar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acepon) from <i>Corynebacterium glutamicum</i> ." <i>Eur J Biochem.</i> 254(2):395-403 (1998)
AJ238250	ndh		Lichinger, T. et al. "Biochemical and biophysical characterization of the cell wall protein of <i>Corynebacterium glutamicum</i> . The channel is formed by a low molecular mass polypeptide." <i>Biochemistry.</i> 37(43):15024-15032 (1998)
AJ238203	porA	Porin	Venes, A. A. et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ." <i>Mol Microbiol.</i> 11(4):739-746 (1994)
DI7429		Transposable element IS31831	

Table 2, Page 3

GenBank® Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the Corynebacterium glutamicum (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142, 3347-3354 (1996)
E01358	hdh, hik	Lamotidine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon Leader peptide; anthranilate synthase	Matsuji, K. et al. "Tryptophan operon, peptide and pliocin coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01376	trpL, trpL	Promoter and operator regions of tryptophan operon	Matsuji, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01377		Biotin synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 199278088-A 1 10/02/92
E03937		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diamino pelargonic acid aminotransferase and deshiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04040		Deshiobiotin synthetase	Kohama, K. et al. "Gene coding diamino pelargonic acid aminotransferase and deshiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041			Kurusu, Y. et al. "Gene DNA coding aspartate and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04307		Flavum asparatase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993076352-A 2 03/30/93
E04484		Prephenate dehydratase	Saitoichi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993184366-A 1 07/27/93
E05108		Aspartokinase	Fujimoto, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipiclorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipiclorinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93

Table 2, Page 4

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E05776	Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent. JP 1993284970. A 1 11/02/93	
E05779	Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent. JP 1993284972. A 1 11/02/93	
E06110	Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent. JP 1993344881. A 1 12/27/93	
E06111	Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent. JP 1993344881. A 1 12/27/93	
E06146	Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent. JP 1993144893. A 1 12/27/93	
E066825	Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent. JP 1994062866-A 1 03/08/94	
E066826	Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent. JP 1994062866-A 1 03/08/94	
E066827	Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent. JP 1994062866-A 1 03/08/94	
E07701	secY	Honno, N. et al. "Gene DNA participating in integration of membrane protein to membrane," Patent. JP 1994169780. A 1 06/21/94	
E08177	Aspartokinase	Saito, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent. JP 1994261766. A 1 09/20/94	
E08178	Feedback inhibition-released Aspartokinase	Saito, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent. JP 1994261766. A 1 09/20/94	
E08179, E08180, E08181, E08182			
E08232	Acetohydroxy-acid isomerase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomerase," Patent. JP 199427067. A 1 10/04/94	
E08234	secE	Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent. JP 199427073. A 1 10/04/94	
E08643	F7 aminotransferase and desulphobiotin synthetase promoter region	Iitakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent. JP 1995031476. A 1 02/03/95	
E08646	Biotin Synthetase	Iitakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent. JP 1995031476. A 1 02/03/95	

Table 2, Page 5

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E08649	Aspartase	Kohama, K. et al "DNA fragment having promoter function in coryneform bacterium," Patent. JP 1995031478-A 1 02/03/95	
E08900	Dihydrodipicolinate reductase	Maddii, M. et al "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent. JP 1995075578-A 1 03/20/95	
E08901	Diaminopimelic acid decarboxylase	Maddii, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent. JP 1995055579-A 1 03/20/95	
E12594	Serine hydroxymethyltransferase	Itayakeyama, K. et al. "Production of L-hypophan," Patent. JP 1997028391-A 1 02/04/97	
E12760, E12759,	transposase	Moriya, M. et al "Amplification of gene using artificial transposon," Patent. JP 1997070291-A 03/11/897	
E12758	Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent. JP 1997070291-A 03/11/897	
E12764	Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent. JP 1997070291-A 03/11/897	
E12767	aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent. JP 1997070291-A 03/11/897	
E12770	Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent. JP 1997070291-A 03/11/897	
E12773	Glucose-6-phosphate dehydrogenase	Itayakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent. JP 1997224661-A 1 09/07/97	
E13655	Thiiconic dehydratase	Mosackel, R. et al. "Functional and structural analysis of the thiorenone dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)	
L01508		Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinohexulosonate-7-phosphate synthase gene," <i>FEBS Microbiol Lett</i> , 107:223-230 (1993)	
L07603	EC 4.2.1.15	Keilhauer, C. et al. "Isolericine synthesis in Corynebacterium glutamicum. molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5593-5603 (1993)	
L09232	IlvB; ilvN; ilvC	Acetoxyhydroxy acid synthase large subunit; Acetoxyhydroxy acid synthase small subunit; Acetoxyhydroxy acid isomeroeductase	

Table 2, Page 6

GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system expression in Escherichia coli and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEBS Microbiol Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H.S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," <i>J Microbiol Biotechnol</i> , 11(4):236-263 (1994)
L27126		Pyruvate kinase	Jeften, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," <i>Appl Environ Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceY	Isocitrate lyase	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dcrR from Brevibacterium lactofermentum," <i>J Bacteriol.</i> , 177(2):465-467 (1995)
L35906	dtxI	Diphtheria toxin repressor	Follette, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum dtxA gene," <i>J Bacteriol.</i> , 167:695-702 (1986)
M13774		Phenylate dehydratase	Paik, Y-H et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J Bacteriol.</i> , 169:1801-1806 (1987)
M1675	5S rRNA		Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	O'Regan, M. et al. "Cloning and nucleotide sequence of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M85106		23S rRNA gene insertion sequence	Rollef, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J Gen Microbiol.</i> , 138:1167-1175 (1992)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
M85107, M85108		23S rRNA gene insertion sequence	Rollei, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992).
M89931	accD; umQ; yhhw	Beta C-S lyase, branched chain amino acid uptake carrier, hypothetical protein yhhw	Rossol, I. et al. "The <i>Corynebacterium glutamicum</i> accD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoluteine uptake in <i>Corynebacterium glutamicum</i> ATCC 13032 is directed by the bmrQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998).
SJ9299	tp	LacZ1 gene (promoter)	Henry, D.M. et al. "Cloning of the tp gene cluster from a tryptophan hyperproducing strain of <i>Corynebacterium glutamicum</i> : identification of a mutation in the tp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993).
UJ1545	tpD	Anthranilate phosphoribosyltransferase	O'Gara, J.P. and Dunigan, L.K. (1994) Complete nucleotide sequence of the <i>Corynebacterium glutamicum</i> ATCC 21850 tpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
UJ3922	cglIM; cglIR; cglQR	Putative type II S-cysteine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schaefer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from <i>Corynebacterium glutamicum</i> ATCC 13032 and analysis of its role in intergeneric conjugation with <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schaefer, A. et al. "The <i>Corynebacterium glutamicum</i> cglIM gene encoding a S-cysteine in an MrBC-deficient <i>Escherichia coli</i> strain," <i>Gene</i> , 203(2):95-101 (1997).
UJ4965	recA		Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996).
UJ1224	px		Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> glutamine biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996).
UJ1225	proC	L-proline NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996).
UJ1230	objg; proB; unkdh	?gamma glutamyl kinase similar to D. isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996).

GenBank™ Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Serebrenikin, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylbacterillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thrR, accBC	"Thiosulfate sulfotransf erase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch Microbiol</i> , 166(2):76-82 (1996)
U43535	cml	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J Bacteriol</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5'-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	Matsuji, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol Gen Genet</i> , 212(1):112-119 (1988)
X07363	lys A	DAT decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant Mol. Biol.</i> , 21 (3):487-502 (1992)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Von den Osten, C.H. et al. "Molecular cloning, nucleotide sequence and functional analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of C. glutamicum fructose 1,6-biphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol</i> .
X17113	ida	Fructose-bisphosphate aldolase	Bonnascie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)
X53393	dapV	1,2,3-dihydroxypropanoate synthetase (EC 4.2.1.52)	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		AntB-related site	Cianciotto, N. et al. "DNA sequence homology between all B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the antP site of lambda corynephage," <i>FEMS Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcoli, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum lysA</i> gene," <i>Mol. Microbiol.</i> , 4(11): 1819-1830 (1990)
X55994	trpL; trpF	Putative leader peptidase, anthranilate synthase component 1	Ierrey, D.M. et al. "Nucleotide sequence of the <i>Corynebacterium glutamicum</i> trpL gene," <i>Nucleic Acids Res.</i> , 18(23): 7138 (1990)
X56037	thrC	Threonine synthase	Ilan, K.S. et al. "The molecular structure of the <i>Corynebacterium glutamicum</i> threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10): 1693-1702 (1990)
X56075		Attachment site	Cianciotto, N. et al. "DNA sequence homology between all B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the antP site of lambda corynephage," <i>FEMS Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartate beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 5(15): 1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in <i>Corynebacterium glutamicum</i> ," <i>Mol. Gen. Genet.</i> , 224(3): 317-324 (1990)
X59403	gap,pck; ipi	Glyceraldehyde-3-phosphate phosphoglycerate kinase, triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a <i>Corynebacterium glutamicum</i> gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19): 6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3): 317-326 (1992)
X60312	lysI	L-lysine permease	Sepp, Feldhaus, A. H. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12): 2995-3005 (1991)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	cop1	Isp protein	Joliff, G. et al. "Cloning and nucleotide sequence of the <i>csp1</i> gene encoding PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i> : The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16), 2349-2362 (1992)
X66112	gli	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the <i>Corynebacterium glutamicum gliA</i> gene encoding citrate synthase," <i>Microbiol.</i> , 140, 1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	Peyrel, J.L. et al. "Characterization of the <i>cspB</i> gene encoding PS2, an ordered surface-layer protein in <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 9(1), 97-109 (1993)
X69103	csp2	Surface layer protein PS2	Bonamy, C. et al. "Identification of IS1206, a <i>Corynebacterium glutamicum</i> IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3), 571-581 (1994)
X69104		IS3 related insertion element	Patek, M. et al. "Leucine synthesis in <i>Corynebacterium glutamicum</i> : enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1), 133-140 (1994)
X70959	leuV	Isopropylmalate synthase	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the <i>Corynebacterium glutamicum</i> icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3), 774-782 (1995)
X71489	icd	Isocitrate dehydrogenase (NADP+)	
		Glutamate dehydrogenase (NADP+)	Heery, D.M. et al. "A sequence from a tryptophan-hypocproline producing strain of <i>Corynebacterium glutamicum</i> encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 20(3), 1255-1262 (1994)
X72855	GDIIA	5-methyltryptophan resistance	Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of <i>Corynebacterium glutamicum</i> and <i>Brevibacterium lactosfermentum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 42(4), 575-580 (1994)
X75083,	mttA		Reinschkeid, D.J. et al. "Characterization of the isochorismate lyase gene from <i>Corynebacterium glutamicum</i> and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12), 3474-3483 (1994)
X75084,			Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X75085	iccA	Partial isocitrate lyase; ?	
X75504	aceA, thiX		
X76875		ATPase beta subunit	

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
X77034	wif	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64: 285-305 (1993)
X77384	rccA		Billman-Moore, H. "Nucleotide sequence of a rccA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6): 403-404 (1994)
X78491	accB	Malate synthase	Reinschütz, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> : sequence analysis," <i>pl-aac operon encoding phosphotransacetylase: sequence analysis</i> ," <i>Microbiology</i> , 140:3039-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, P.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Nocardioides</i> and evidence for the evolutionary origin of the genus <i>Nocardioides</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronemeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinylaminopimelate desuccinylase	Wehmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 140:3349-3356 (1994)
X82061		16S ribosomal RNA	Ruijter, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebirska, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebirska, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann, A. et al. "Functional analysis of sequences adjacent to dapE of <i>Corynebacterium glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transport," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
X86157	aigB; aigC; argD; aigF; aigJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> ; 142:99-108 (1996)
X89084	piu; ackA	Phosphate acetyltransferase, acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> piu-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> ; 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AΔ12 infecting 'Arthrobacter aurus' C70," <i>J. Bacteriol.</i> 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90360		Promoter fragment F22	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
X90363	Promoter fragment F45	Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364	Promoter fragment F64	Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365	Promoter fragment F75	Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366	Promoter fragment PF101	Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367	Promoter fragment PF104	Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368	Promoter fragment PR109	Promoters from <i>Corynebacterium glutamicum</i> : cloning, ammonium uptake carrier of <i>Corynebacterium glutamicum</i> , " <i>J Biol Chem</i> , 271(10):5398-5403 (1996)	Siewe, R. M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J Biol Chem</i> , 271(10):5398-5403 (1996)
X93513	am1	Glycine betaine transport system	Petei, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J Bacteriol</i> , 178(17):5229-5234 (1996)
X93514	betP	Glycine betaine transport system	Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORE2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biootechnol Lett</i> , 19:1113-1117 (1997)
X93649	orf4	Lysine exporter protein, L-lysine export regulator protein	Vrijic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol Microbiol</i> , 22(5):815-826 (1996)
X96471	LysE, LysG	Lysine exporter protein, L-lysine export regulator protein	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X96580	panB, panC, xyfB	3-methyl-2-oxobutanate hydroxymethyltransferase, pantoate-bctB-alanine ligase; xylose kinase	Sahin, H. et al. "D-pantothenic synthesis in <i>Corynebacterium glutamicum</i> and use of panBC and genes encoding L-valine synthesis for D-pantothenic overproduction," <i>Appl Environ Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer <i>Brevibacterium lactofermentum</i> (<i>Corynebacterium glutamicum</i> ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
X99289		Elongation factor P	Malcos, J. M. et al. "Nucleotide sequence of the homoserine kinase (thiB) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00140	thiB	Homoserine kinase	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Malcos, J. M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thiA) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00476	thiA	Homoserine dehydrogenase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the <i>Corynebacterium glutamicum</i> hom-thiB operon," <i>Mol Microbiol.</i> , 2(1):63-72 (1988)
Y00546	hom; thiB	Homoserine dehydrogenase; homoserine kinase	Homuthia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from <i>Brevibacterium lactofermentum</i> ," <i>Mol Gen Genet.</i> , 259(1):97-104 (1998)
Y08964	murC, ftsQDivD, ftsZ	UDP-N-acetylglucosamine-ligase, division initiation protein or cell division protein; cell division protein	Peter, H. et al. "Isolation of the pufP gene of <i>Corynebacterium glutamicum</i> proline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch Microbiol.</i> , 168(2):143-151 (1997)
Y09163	pufP	High affinity proline transport system	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from <i>Corynebacterium glutamicum</i> : characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09548	pyc	Pyruvate carboxylase	Paick, M. et al. "Analysis of the leuB gene from <i>Corynebacterium glutamicum</i> ," <i>Appl Microbiol Biotechnol.</i> , 50(1):42-47 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Moreau, S. et al. "Site-specific integration of coryncophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)
Y12472		Attachment site bacteriophage Phi-16	

Table 2, Page 15

GenBank™ Accession No.	Gene Name	Gene Function	Reference
Y12537	proP	Proline/citidine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes. Identification, sequencing, and characterization of the proline/citidine uptake system, ProP, and the citidine/proline/glycine betaine carrier, CtpP." <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of Corynebacterium glutamicum glnA gene encoding Glutamine synthetase I." <i>FEBS Microbiol Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrodipicolinate dehydrogenase	Moréau, S. et al. "Analysis of the integration functions of & phi;304L. An integrase module among corynophages." <i>Virology</i> , 255(1): 150-159 (1999)
Y18059		Attachment site Corynephage 304L	Oguiza, J. A. et al. "A gene encoding arginyl tRNA synthetase is located in the upstream region of the lysA gene in Brevibacterium lactofermentum." <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
221501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of Brevibacterium lactofermentum encodes dihydroadipicollinate reductase, and a third polypeptide of unknown function." <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
221502	dapA; dapB	Dihydroadipicollinate synthase; dihydroadipicollinate reductase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase." <i>Appl Environ Microbiol.</i> , 60(7):2209-2219 (1994)
229563	thrC	Threonine synthase	Oguiza, J. A. et al. "Multiple sigma factor genes in Brevibacterium lactofermentum. Characterization of sigA and sigB." <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
246753	16S rDNA	Gene for 16S ribosomal RNA	Oguiza, J. A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of Brevibacterium lactofermentum is coupled transcriptionally to the dmdR gene." <i>Gene</i> , 177:103-107 (1996)
249822	sigA	SigA sigma factor	Oguiza, J. A. et al. "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB." <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
249823	galE; dmdR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein ?; SigB sigma factor	Corcua, A. et al. "Cloning and characterization of an IS-like element present in the genome of Brevibacterium lactofermentum ATCC 13869." <i>Gene</i> , 170(1):91-94 (1996)
249824	orf1; sigB		A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.
266334		Transposase	

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

GENUS	SPECIES	STRAIN	PATENT NUMBER	NAME
Brevibacterium	ammoniagenes	21054		
Brevibacterium	ammoniagenes	19350		
Brevibacterium	ammoniagenes	19351		
Brevibacterium	ammoniagenes	19352		
Brevibacterium	ammoniagenes	19353		
Brevibacterium	ammoniagenes	19354		
Brevibacterium	ammoniagenes	19355		
Brevibacterium	ammoniagenes	19356		
Brevibacterium	ammoniagenes	21055		
Brevibacterium	ammoniagenes	21077		
Brevibacterium	ammoniagenes	21553		
Brevibacterium	ammoniagenes	21580		
Brevibacterium	ammoniagenes	39101		
Brevibacterium	butanicum	21196		
Brevibacterium	divaricatum	21792	1928	
Brevibacterium	flavum	21474		
Brevibacterium	flavum	21129		
Brevibacterium	flavum	21518		
Brevibacterium	flavum		B11474	
Brevibacterium	flavum		B11472	
Brevibacterium	flavum	21127		
Brevibacterium	flavum	21128		
Brevibacterium	flavum	21427		
Brevibacterium	flavum	21475		
Brevibacterium	flavum	21517		
Brevibacterium	flavum	21528		
Brevibacterium	flavum	21529		
Brevibacterium	flavum	B11477		

<i>Brevibacterium flavum</i>				B11478
<i>Brevibacterium flavum</i>	<i>flavum</i>	21127		
<i>Brevibacterium flavum</i>	<i>flavum</i>			B11474
<i>Brevibacterium lacali</i>		15527		
<i>Brevibacterium keoglutamicum</i>		21004		
<i>Brevibacterium keoglutamicum</i>		21089		
<i>Brevibacterium ketosoreducum</i>		21914		
<i>Brevibacterium lactofermentum</i>			70	
<i>Brevibacterium lactofermentum</i>			74	
<i>Brevibacterium lactofermentum</i>			77	
<i>Brevibacterium lactofermentum</i>				
<i>Brevibacterium lactofermentum</i>		21798		
<i>Brevibacterium lactofermentum</i>		21799		
<i>Brevibacterium lactofermentum</i>		21800		
<i>Brevibacterium lactofermentum</i>		21801		
<i>Brevibacterium lactofermentum</i>			B11470	
<i>Brevibacterium lactofermentum</i>			B11471	
<i>Brevibacterium lactofermentum</i>		21086		
<i>Brevibacterium lactofermentum</i>		21420		
<i>Brevibacterium lactofermentum</i>		21086		
<i>Brevibacterium lactofermentum</i>		31269		
<i>Brevibacterium linens</i>		9174		
<i>Brevibacterium linens</i>		19391		
<i>Brevibacterium linens</i>		8377		
<i>Brevibacterium parafinolyticum</i>			11160	
<i>Brevibacterium spec.</i>				717.73
<i>Brevibacterium spec.</i>				717.73
<i>Brevibacterium spec.</i>				
<i>Brevibacterium spec.</i>		14604		
<i>Brevibacterium spec.</i>		21860		
<i>Brevibacterium spec.</i>		21864		
<i>Brevibacterium spec.</i>		21865		
<i>Brevibacterium spec.</i>		21866		
<i>Brevibacterium spec.</i>		19240		

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Corynebacterium	acecticidophilum	21476
Corynebacterium	acecticidophilum	13870
Corynebacterium	acecoglutamicum	B11473
Corynebacterium	acecoglutamicum	B11473
Corynebacterium	acecoglutamicum	15806
Corynebacterium	acecoglutamicum	21491
Corynebacterium	acecoglutamicum	31270
Corynebacterium	acecoglutamicum	B33671
Corynebacterium	acecophilum	2399
Corynebacterium	ammoniogenes	6872
Corynebacterium	ammoniogenes	15511
Corynebacterium	fujikense	21496
Corynebacterium	glutamicum	14067
Corynebacterium	glutamicum	39137
Corynebacterium	glutamicum	21254
Corynebacterium	glutamicum	21255
Corynebacterium	glutamicum	31830
Corynebacterium	glutamicum	13032
Corynebacterium	glutamicum	14305
Corynebacterium	glutamicum	15455
Corynebacterium	glutamicum	13058
Corynebacterium	glutamicum	13059
Corynebacterium	glutamicum	13060
Corynebacterium	glutamicum	21492
Corynebacterium	glutamicum	21513
Corynebacterium	glutamicum	21526
Corynebacterium	glutamicum	21543
Corynebacterium	glutamicum	13287
Corynebacterium	glutamicum	21851
Corynebacterium	glutamicum	21253
Corynebacterium	glutamicum	21514
Corynebacterium	glutamicum	21516
Corynebacterium	glutamicum	21299

Corynebacterium	Glutamicum	21300
Corynebacterium	Glutamicum	19664
Corynebacterium	Glutamicum	21488
Corynebacterium	Glutamicum	21649
Corynebacterium	Glutamicum	21650
Corynebacterium	Glutamicum	19223
Corynebacterium	Glutamicum	13869
Corynebacterium	Glutamicum	21157
Corynebacterium	Glutamicum	21158
Corynebacterium	Glutamicum	21159
Corynebacterium	Glutamicum	21155
Corynebacterium	Glutamicum	31808
Corynebacterium	Glutamicum	21674
Corynebacterium	Glutamicum	21562
Corynebacterium	Glutamicum	21563
Corynebacterium	Glutamicum	21564
Corynebacterium	Glutamicum	21565
Corynebacterium	Glutamicum	21566
Corynebacterium	Glutamicum	21567
Corynebacterium	Glutamicum	21568
Corynebacterium	Glutamicum	21569
Corynebacterium	Glutamicum	21570
Corynebacterium	Glutamicum	21571
Corynebacterium	Glutamicum	21572
Corynebacterium	Glutamicum	21573
Corynebacterium	Glutamicum	21579
Corynebacterium	Glutamicum	19049
Corynebacterium	Glutamicum	19050
Corynebacterium	Glutamicum	19051
Corynebacterium	Glutamicum	19052
Corynebacterium	Glutamicum	19053
Corynebacterium	Glutamicum	19054

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<i>Corynebacterium</i>	<i>glutamicum</i>	19055
<i>Corynebacterium</i>	<i>glutamicum</i>	19056
<i>Corynebacterium</i>	<i>glutamicum</i>	19057
<i>Corynebacterium</i>	<i>glutamicum</i>	19058
<i>Corynebacterium</i>	<i>glutamicum</i>	19059
<i>Corynebacterium</i>	<i>glutamicum</i>	19060
<i>Corynebacterium</i>	<i>glutamicum</i>	19185
<i>Corynebacterium</i>	<i>glutamicum</i>	13286
<i>Corynebacterium</i>	<i>glutamicum</i>	21515
<i>Corynebacterium</i>	<i>glutamicum</i>	21527
<i>Corynebacterium</i>	<i>glutamicum</i>	21544
<i>Corynebacterium</i>	<i>glutamicum</i>	21492
<i>Corynebacterium</i>	<i>glutamicum</i>	B8183
<i>Corynebacterium</i>	<i>glutamicum</i>	B8182
<i>Corynebacterium</i>	<i>glutamicum</i>	B12416
<i>Corynebacterium</i>	<i>glutamicum</i>	B12417
<i>Corynebacterium</i>	<i>glutamicum</i>	B12418
<i>Corynebacterium</i>	<i>glutamicum</i>	B11476
<i>Corynebacterium</i>	<i>glutamicum</i>	21608
<i>Corynebacterium</i>	<i>glutamicum</i>	P973
<i>Corynebacterium</i>	<i>lilium</i>	11594
<i>Corynebacterium</i>	<i>nitrilophilus</i>	21419
<i>Corynebacterium</i>	<i>spec.</i>	P4445
<i>Corynebacterium</i>	<i>spec.</i>	P4446
<i>Corynebacterium</i>	<i>spec.</i>	31088
<i>Corynebacterium</i>	<i>spec.</i>	31089
<i>Corynebacterium</i>	<i>spec.</i>	31090
<i>Corynebacterium</i>	<i>spec.</i>	31090
<i>Corynebacterium</i>	<i>spec.</i>	31090
<i>Corynebacterium</i>	<i>spec.</i>	20145
<i>Corynebacterium</i>	<i>spec.</i>	15954
<i>Corynebacterium</i>	<i>spec.</i>	21857
<i>Corynebacterium</i>	<i>spec.</i>	21862
<i>Corynebacterium</i>	<i>spec.</i>	21863
<i>Corynebacterium</i>	<i>spec.</i>	

- ATCC: American Type Culture Collection, Rockville, MD, USA
FERMI: Fermentation Research Institute, Chiba, Japan
NRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA
CECT: Colección Española de Cultivos Típicos, Valencia, Spain
NCIMB: National Collection of Industrial and Marine Bacteria Ltd, Aberdeen, UK
CBS: Centraalbureau voor Schimmelcultures, Baarn, NL
NCITC: National Collection of Type Cultures, London, UK
DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany
For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms. Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saitama, Japan.

>>RXA01017-amino acid sequence
(1-609, translated) 203 residues

MAQKVTFWFD TTCPPFCWVTS RWIKEVEQVR DIEIQWVPM S LAVLNEGRDL PEDYKERMKA AWGPARVFAA
VATDHADKLG DLYTAMGTRI HNDGRGPPIEG SFNDVIAEAL EEVGLDAALG EVADTTEWDD ALRAFHQTAM
DEVGNDVGT P VVKLGDTAFF GPVLTRIPRG EEAGEIFDAS FKLASYPHFF EIKRSRTENP QFD

>RXA01017-nucleotide sequence A: upstream

GAATTTGAGGGGGCGCTACCCCTAGAACGGTGC GCAATGACACCACGATA GTTCGCCCTAGTGTGGATTGCTAGAA
AACTTTAAGAAAGAGGAAATAAT

>RXA01017-nucleotide sequence B: coding region

ATGGCTCAAAAGTAACCTCTGGTCGATACCACCTGCCATTCTGCTGGTCACCTCCGCTGGATTAAAGGAAGT
CGAACAAAGTCCCGCATATTGAAATCCAGTGGGTCCAATGAGCCTCGCTCTAAACGAACGGCGTGATCTCCCAG
AGGATTACAAGGAGGCCATGAAGGCTGCATGGGGAC CAGCACCGCTTTCG CAGCTGTCGCCACCGACCATGCTGAC
AAGCTCGCGACCTGTACACCGCAATGGGTACCCGCATCCACAACGACGGTCGGACCAATCGAAGGTTCTCAA
TGATGTCACTCGCAGAGGC ACTTGAAGAGGTGGCCTAGACCGCTGCACTTGGTGAAGTTGCAGACACCACCGAATGGG
ACGACGCACTTCGCGATTCCACCAGACCGCAATGGACGAGGTGGCAACGATGTGGAACCCAGTGGTCAAGCTC
GGCGACACCGCTTCTCGGCCAGTGCTACCCGCATCCCACCGCGAGGAAGCAGGAGAGATCTCGACGCTTC
CTTCAAGCTCGCAAGCTATCCCCACTTCTTGAATCAAGCGCAGCCGCACTGAGAACCCACAGTTCGAC

>RXA01017-nucleotide sequence C: downstream

TAATTAACGCTGTCTGCTTAT

>>RXA01021-amino acid sequence
(1-522, translated) 174 residues

MSSSESSRSE GSQPAPSVQP ERRADSTGAP AAASKEASQQ MDAAGVLEWA RTAVEQLSER RAEINALNVE
PVPDADTGSN MTYTMATAALD EALKLGELGD VARITEALAV GSVRGARGNS GVVLSQVLRA IAQAAADGVI
DGHTIQEALS IARSLVDRAI TDPVEGTVVTT VLRS

>RXA01021-nucleotide sequence A: upstream

CGAGAGGCCTTTGGCTCTAACGCCCTTTAGTCGTGCGAACGAAATCTTAAGCAGCCTCGGTGCCACCGAGATCGAT
TGGTCGCTGTAAGGTATCTGATT

>RXA01021-nucleotide sequence B: coding region

ATGTCCAGTTCCGAAAGCTCGCGTTCCGAAGGCTCGCAGCCAGCACCCTGTACAGCCTGAACGCCGTGCTGATTCA
AACGGGGGCTCTCGCGCAGCTCCAAGGAAGCTCCAAACAAATGGACGCTGCCGGAGTTCTTGAGTGGGCCAGGA
CCGCTGTGGAGCAGCTTCTGAACGTCGTGCAGAGATCAATGCACTGAATGTCTTCCTGTTCCAGATGCAGACACT
GGATCAAACATGACCTACACCATGACAGCTGCGTTGGATGAAGCGCTGAAACTGGGGAGTTGGGTGATGTCGCAAG
GATTACTGAGGCTTGGCTGTTGGTTCTGTGCGTGGAGCCCCGAGGAATCTGGAGTAGTCCTTAGTCAGGTCTTC
CGCCTATTGCTCAGGCAGCTGCTGACGGGTTATTGATGGCCACACAATCCAAGAAGCGCTATCCATTGCTCGCTCC
CTAGTTGATCGCGCAATTACAGATCCTGTGGAGGGCACTGTTGTCACTGTGTTGCGTTCT

>>RXA01074-amino acid sequence
(1-705, translated) 235 residues

LAEAAGLRWL AEASSAVAQV VSADAEQITT VGVETQLPTP DAAFKAGEEL ARIHLAGAPA FGCPPAGWAG
LNYIGTQGQA CLSTPTWGVF YSQQRVLPAF RRARRRNHLT EHAWVVEAA CDLISELPDD VPPARIHGDL
WFGNLLFGTD GPVFIDPAAH GGHPETDLAM LDVFGAPYLD EIREGYLSIN PLPDGWRERT PMHQLHPLAV
HAASHGPSYG VELLHAAKAT LKLLD

>RXA01074-nucleotide sequence A: upstream

CGAATGAAATCACTGGCGGGAGTCACCCCTCGCGAGGAGCCTGAGCGCTACTAGCTTGCCACATTCACTAAC
GCCCGCGACAACCCCAAGCAGCC

>RXA01074-nucleotide sequence B: coding region

TTGGCGGAAGCCGCAGGTCTACGCTGGCTGCCGAAGCATCTCAGCTGGCACAGGTTGTTAGCGCCGACCCAGA
GCAGATCACGACTGTTGGCGTCGAAACGCAATTGCCACACCCGATGCCCTCAAGGCCGGCGAAGAGCTGCC
GCATCCACCTTGCCGGCCCCAGCGTCTGGCTGTCCACCAGCGGGCTGGCGGGGTTAAACTACATCGGCACCCAG
GGACAAGCATGCTTATCGACCCCCACCTGGGGTGTTTTACTCCCAGCAACCGTACTCCGTTGCGGCCGGGC
ACCCAGGCCAAATCACCTCACCGAGCACGACTCTGGGCGTGGAAAGCCGCTGTGATTGATTAGCGAACTCCCG
ATGACGTTCCCCCGCCAGAACCTCACGGCGACTTGTGGTTGGCAACCTACTTTGGCACAGACGGCCGTGTTT
ATTGACCCCCGAGCTCACGGCGTCACTGGGAAACTGATCTCGCGATGCTGATGTATTGGCGCACCCATGCACCAACTCC
TGAATCCGGGAAGGTTATCTGTCTATCAACCCGCTGCCAGACGGGTGGCGTGAACGCACCCATGCACCAACTCC
ACCCCTTGCCGTACATGCCGTCTCATGGCCAAGCTACGGCGTGGAACTACTCCACGCCGCAAAGCGACACTC
AAACTGTTGGAT

>RXA01074-nucleotide sequence C: downstream

TAACGCCACCAATTTCCTGCGG

>>RXA01078-amino acid sequence

(1-834, translated) 278 residues

MSNAVPHNVS FN FVPRAYRP EKPRTFGMTE IRAPYYSTFG TRHLQDVFDV AGQWVDGIKW AGGSFSLVPT
EQVRAFSDIA HENNAVSSG GWIETVLRYG DDAVDHYLKE AKEVGFDVIE ISTGFIMLNT SGLQLVKEKV
VKAGLKAKPE LGLQIGSGGD SGEAELAAEG KKDI GDLVDR GKKALDAGAS IIMIESEGIT ENVTEWDTGA
AAASIINGLGL ENVMFEAADG PVFEWYVKNY GNECNLFVDH SQILQLEGLR QNIWGNKSTW GRVINPAP

>RXA01078-nucleotide sequence A: upstream

ATCATTCA CGAGCTCGATAGCCGACAGGTTCTGA ACTCACAGAAGCCCTGGCAAAGTCTCCACCACCCGAGCTA
AAACTTTGAAAGGAGCTCATC

>RXA01078-nucleotide sequence B: coding region

ATGAGCAACCGCAGTACCCACAACGTTCTCAACTTGTTCGGCGCTTACCGTCCAGAAAAGCCCCGCACATT
CGGCATGACAGAAATTCTGTGCACCGTACTACTCCACTTCGGCACCCGACACCTCCAGGATGTCATGTTGCAG
GCCAGTGGGTGGACGGCATCAAATGGCAGGCGGTTCTCTCCCTGGTGGCCGACCGAACAGTGCCTGCTTTAGC
GACATGCCATGAAAACAATGCCTATGTGCTTCCGGTGGATTGAAACTGTGCTTCGCTACGGCGACGACGC
AGTTGATCATTACTAAAGGAAGCCAAGGAAGTCGGCTTCGATGTTATTGAGATTCCACGGATTCA TCA TGC
ACACTTCAGGTCTTCAGCGCTGGTAGAAAAAGTGGTCAAGGCAGGCCTCAAAGCAAAACCTGAACTAGGACTACAG
ATTGGTTCCGGAGGCAGCTGGTGGACTCTGGTGGACTGGTCAACTTGCAAGCCGAAGGAAAGAACATTGGC
CGTAAAAAAGCTCTCGACGCCGCATCCATCATGATCGAATCCGAAAGGCATACCGAAAACGTACCGAAT
GGGATACAGCGCTGCCGCTCATCAATGGACTGGATTAGAAAACGTATGTTCGAAGCCGCCGACGGCCCC
GTCTTGAGTGGTATGTCAAAAACACGGCAACGAATGCAACCTGTCGACCACAGTCAAATTCTGCAACTTGA
AGGGCTGCGCCAAAACATCTGGGCAACAAGACACCTGGGACGAGTAATCAACCCTGCGCCT

>RXA01078-nucleotide sequence C: downstream

TAAATACCAGGTCAAGGGAGGGCA

>>RXA01088-amino acid sequence

(1-1182, translated) 394 residues

MGLWIDATAG VAGDMILLGAL IDAGAELEKI QQVVEAVIPG DVLLRTEEVV RQGORGKILH VDAQHEHHHH
RHLSTIKELL VNADIPEQTK QDALGVFELI AIAEGKVHGI EPEKIHFHEV GAWDSIADIV GVCEAIRQLN
PGLLIAASPIA LGFGRIKAH GDIPVPVPAV AELVKGWPTQ TGALMESTEP VGELETPTGV ALIRHFATQD
GPFPGGIINE VGIGAGTKDT EGRPNIVRAI LFNTSRSNPD TRTLVQLEAN VDDQDPRLWP GVIEILFAAG
AVDAWLTPIL MKKGRPAHRV SALVDSSEVE AVKTALFAAT TTGIRSWEV EREGLDRRFE QVEDGHTIN
IKIGSRDDQV ISAQSEFEDI RSAAVALGIS EREVVARIPQ GTTE

>RXA01088-nucleotide sequence A: upstream

TGCCTTGAGTCTAATTCTCCCGCCGTGCGATGGGTTAACGCTGGACTGATAAACCTTTGTGAACCGAATTTTA
ACTGATTTGAAGAACCGAGAATA

>RXA01088-nucleotide sequence B: coding region

ATGGGACTGTGGATCGAACCGCTGGCGTTGCAGGGATATGTTGCTGGGAGCACTCATTGATGCAGGTGCAGA
ACTAGAAAAAAATCCAACAGGTTGGAAGCAGTCATCCCCGGTACGTGCTCTTGCACCCGAAAGAGGTAGTGC
AAGGCCAACGAGGCATCAAGCTGCATGTGGACGCACAAACATGAACACCACATCACCCCACTTAAGCACCATTAAA
GAACCTGCTGTCAATGCTGACATCCCTGAACAAACCAAGCAGGATGCCTTAGGCCTTTGAACTCATCGTATCG
TGAAGGAAAAGTCCACGGCATCGAGCCGGAGAAAATCCACTTCCATGAGGTAGGAGCTGGGATTCCATCGCAGACA
TTGTGGGTGTGCGAAGCGATCAGGAGCTTAACCCAGGTTGATTGCTGCATCTCCGATTGCTTTAGGATTCGGA
CGCATCAAGGCAGCTCACGGAGATATTCCAGTGCCTCCAGCGTGGCAGAGCTGGTGAAGGCTGGCCACCC
AACCGGAGCTTATGGAGAGCACCGAACCTGTTGGTAATTAGCCACCCAACTGGTGTGCGTTGATCCGTACT
TTGCCACCCAAAGATGCCCTTCCCAGGTGGCATCATCAATGAAGTGGCATTGGTCAGGAACAAAGATACAGAA
GCCCGTCCAATATAGTGCAGCAATTGTTCAACACCTCTAGGAGTAACCCAGATAACCGCACACTGGTCAATT
AGAAGCCAATGTTGATGATCAAGACCCACGGCTGTGGCCAGGAGTAATAGAGATCCTTTGCCCTGGCCAGTAG
ATGCATGGCTGACTCCAATTGATGAAGAAGGGCCCTGCACATACGGTGTCACTGGTGGATAGCTCCGAG
GTGGAAGCAGTGAAACCGCATTATTGCACCCACCAAGCTTGGGATCAGATCATGGGAAGTCGAACCGAGAAGG
CTTGGACCGTCGTTCGAACAGTCGAGGTGGACGGACACACCATCAACATCAAATCGGTTCCGTGATGATCAAG
TAATCAGTGCACAGTCGAGTTGAAGATATTGGTCTGCAGCGGTGGCCTGGAAATTTCAGAGCGGGAGTTGTC
GCAAGAATTCCGCAAGGCACCCACCGAG

>RXA01088-nucleotide sequence C: downstream

TAACAAACCAAAAGGTGACTGCT

(10) 100-000

Claims

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an MCP protein, or a portion thereof.
- 5 2. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule encodes an MCP protein involved in fine chemical production.
- 10 3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof.
4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth in Appendix B.
- 15 5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth in Appendix B.
- 20 6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof.
- 25 7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth in Appendix A.
8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
- 30 9. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 1-8 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.
10. A vector comprising the nucleic acid molecule of any one of claims 1-9.
- 35 11. The vector of claim 10, which is an expression vector.
12. A host cell transfected with the expression vector of claim 11.
- 40 13. The host cell of claim 12, wherein said cell is a microorganism.
14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
- 45 15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.

16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, and enzymes.
- 5 17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.
- 10 18. An isolated MCP polypeptide from *Corynebacterium glutamicum*, or a portion thereof.
- 15 19. The polypeptide of claim 18, wherein said polypeptide is involved in fine chemical production.
- 20 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B.
- 25 21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, or a portion thereof.
22. The isolated polypeptide of any of claims 18-21, further comprising heterologous amino acid sequences.
- 25 23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth in Appendix A.
- 30 24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B.
- 35 25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
- 40 27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
- 45 28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*.

Corynebacterium acetophilum. *Corynebacterium ammoniogenes*. *Corynebacterium fujiiokense*. *Corynebacterium nitrilophilus*. *Brevibacterium ammoniagenes*.
5 *Brevibacterium butanicum*. *Brevibacterium divaricatum*. *Brevibacterium flavum*.
Brevibacterium healii. *Brevibacterium ketoglutamicum*. *Brevibacterium ketosoreductum*. *Brevibacterium lactofermentum*. *Brevibacterium linens*.
Brevibacterium paraffinolyticum. and those strains set forth in Table 3.

30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.
10 31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, and enzymes.
15 32. The method of claim 25, wherein said fine chemical is an amino acid.
33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.
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25 34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.